



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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| <b>(54) Title:</b> HUMAN RECEPTOR TYROSINE KINASE, KDR<br><br><b>(57) Abstract</b><br><br>An isolated nucleic acid molecule encoding a novel human receptor type tyrosine kinase gene, KDR, is disclosed. The isolation of this KDR cDNA sequence results in disclosure of purified forms of human KDR protein, recombinant vectors and recombinant hosts which express human KDR.  |           |  |

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## TITLE OF THE INVENTION

HUMAN RECEPTOR TYROSINE KINASE, KDR

## 5 CROSS-REFERENCE TO RELATED APPLICATIONS

This non-provisional application is a continuation-in-part of U.S. Provisional Application Serial No. 60/050,962, filed June 18, 1997.

## STATEMENT REGARDING FEDERALLY-SPONSORED R&amp;D

10 Not applicable

## REFERENCE TO MICROFICHE APPENDIX

Not applicable

## 15 FIELD OF THE INVENTION

The present invention relates to an isolated nucleic acid molecule (polynucleotide) which encodes a human receptor tyrosine kinase, KDR, which is expressed on human endothelial cells. This receptor is activated by VEGF and mediates a mitogenic signal. The present invention also relates to recombinant vectors and recombinant hosts which contain a DNA fragment encoding human KDR, a DNA fragment encoding the intracellular portion of KDR, a DNA fragment encoding the extracellular portion of KDR with or without a membrane anchor sequence, substantially purified forms of associated human KDR, and human mutant forms of KDR.

## BACKGROUND OF THE INVENTION

Vascular endothelial cells form a luminal non-thrombogenic monolayer throughout the vascular system. Mitogens promote embryonic vascular development, growth, repair and angiogenesis in these cells. Angiogenesis involves the proteolytic degradation of the basement membrane on which endothelial cells reside followed by the subsequent chemotactic migration and mitosis of these cells to support sustained growth of a new capillary shoot. One class of mitogens selective for vascular endothelial cells include vascular endothelial growth factor (referred to as VEGF or VEGF-A)

and the homologues placenta growth factor (PlGF), VEGF-B and VEGF-C.

Human VEGF exists as a glycosylated homodimer in one of four mature processed forms containing 206, 189 (see U.S. Patent No. 5,240,848), 165 (see U.S. Patent No. 5,332,671), and 121 (U.S. Patent No. 5,332,671) amino acids, the most prevalent being the 165 amino acid form. The 206 amino acid and 189 amino acid forms of human VEGF each contain a highly basic 24-amino acid insert that promotes tight binding to heparin, and presumably, heparin proteoglycans on cellular surfaces and within extracellular matrices (Ferrara et al., 1991, *J. Cell. Biochem.* 47: 211-218).

Human PlGF is also a glycosylated homodimer which shares 46% homology with VEGF at the protein level. Differential splicing of human PlGF mRNA leads to either a 170 or 149 amino acid residue precursor, which are proteolytically processed to mature forms of 152 or 131 amino acid residues in length, respectively (Maglione et al., 1993, *Oncogene* 8: 925-931; Bayne and Thomas, 1992, EPO Publication No. 0 506 477 A1; Hauser and Weich, 1993, *Growth Factors* 9: 259-268).

VEGF-B has been isolated and characterized (Grimmond et al., 1996, *Genome Research* 6: 124-131; Olofsson et al., 1996, *Proc. Natl. Acad. Sci. USA* 93: 2576-2581). The full-length human cDNAs encode 188 and 207 amino acid residue precursors wherein the NH<sub>2</sub> terminal portions are proteolytically processed to mature forms 167 and 186 amino acid residues in length. Human VEGF-B expression was found predominantly in heart and skeletal muscle as a disulfide-linked homodimer. However, human VEGF-B may also form a heterodimer with VEGF (*id.* @ 2580).

VEGF-C has also been isolated and characterized (Joukov et al., 1996, *EMBO J.* 15: 290-298). A cDNA encoding VEGF-C was obtained from a human prostatic adenocarcinoma cell line. A 32 kDa precursor protein is proteolytically processed to generate the mature 23 kDa form, which binds the receptor tyrosine kinase, Flt-4.

VEGF and its homologues impart activity by binding to vascular endothelial cell plasma membrane-spanning tyrosine kinase receptors which then activate an intracellular mitogenic signal. The

KDR receptor family is the major tyrosine kinase receptor which transduces the mitogenic signal initiated by VEGF.

Shibuya et al. (1990, *Oncogene* 5: 519-524) disclose a human receptor type tyrosine kinase gene *flt*, which comprises a 4.2 Kb open reading frame encoding a 1338 amino acid protein which comprises a glycosylated extracellular domain, membrane spanning region and predicted tyrosine kinase domain.

Pajusola et al. (1992, *Cancer Res.* 52: 5738-5743) disclose a human receptor type tyrosine kinase gene which, as noted above, binds human VEGF-C.

Vascular endothelial growth factor (VEGF) binds the high affinity membrane-spanning tyrosine kinase receptors KDR and Flt-1. Cell culture and gene knockout experiments indicate that each receptor contributes to different aspects of angiogenesis. KDR mediates the mitogenic function of VEGF whereas Flt-1 appears to modulate non-mitogenic functions such as those associated with cellular adhesion. Inhibiting KDR thus significantly diminishes the level of mitogenic VEGF activity.

Vascular growth in the retina leads to visual degeneration culminating in blindness. VEGF accounts for most of the angiogenic activity produced in or near the retina in diabetic retinopathy. Ocular VEGF mRNA and protein are elevated by conditions such as retinal vein occlusion in primates and decreased pO<sub>2</sub> levels in mice that lead to neovascularization. Intraocular injections of either anti-VEGF monoclonal antibodies or VEGF receptor immunofusions inhibit ocular neovascularization in rodent and primate models. Regardless of the cause of induction of VEGF in human diabetic retinopathy, inhibition of ocular VEGF is useful in treating the disease.

Expression of VEGF is also significantly increased in hypoxic regions of animal and human tumors adjacent to areas of necrosis. Monoclonal and polyclonal anti-VEGF antibodies inhibit the growth of human tumors in nude mice. Although these same tumor cells continue to express VEGF in culture, the antibodies do not diminish their mitotic rate of most, if not all, tumor cells derived from cells other than vascular endothelial cells themselves. Thus tumor-derived VEGF does not function as an autocrine mitogenic factor for

most tumors. Therefore, VEGF contributes to tumor growth *in vivo* by promoting angiogenesis through its paracrine vascular endothelial cell chemotactic and mitogenic activities. These monoclonal antibodies also inhibit the growth of typically less well vascularized human colon  
5 cancers in athymic mice and decrease the number of tumors arising from inoculated cells. Viral expression of a VEGF-binding construct of Flk-1, the mouse KDR receptor homologue, truncated to eliminate the cytoplasmic tyrosine kinase domains but retaining a membrane anchor, virtually abolishes the growth of a transplantable glioblastoma in mice  
10 presumably by the dominant negative mechanism of heterodimer formation with membrane-spanning endothelial cell VEGF receptors. Embryonic stem cells, which normally grow as solid tumors in nude mice, do not produce detectable tumors if both VEGF alleles are knocked out. Taken together, these data indicate the role of VEGF in the growth  
15 of solid tumors. KDR and Flt-1 are implicated in pathological neoangiogenesis, and inhibitors of these receptors are useful in the treatment of diseases in which neoangiogenesis is part of the overall pathology, e.g., diabetic retinal vascularization, various forms of cancer as well as forms of inflammation such as rheumatoid arthritis,  
20 psoriasis, contact dermatitis and hypersensitivity reaction.

Terman et al. (1991, *Oncogene* 6: 1677-1683; 1992, *Biochem. Biophys. Res. Commun.* 187: 1579-1586) disclose a full-length cDNA encoding a form of KDR. However, the Terman et al. disclosures do not identify a novel, optimal nucleic acid fragment encoding the human  
25 form of the receptor type tyrosine kinase gene, KDR. It will be advantageous to identify and isolate a human cDNA sequence encoding an optimized form of human KDR. A nucleic acid molecule expressing the human KDR protein will be useful in screening for compounds acting as a modulator of the protein kinase domain of this protein. Such  
30 a compound or compounds will be useful in modulating the mitogenic signal of VEGF and VEGF-related proteins on vascular endothelial cells. The KDR nucleic acid sequence may be also useful for gene therapy encoding a portion of the KDR protein that would contain functional ligand binding and membrane anchoring moieties but not  
35 tyrosine kinase activity. Either all or a portion of the KDR protein is also useful to screen for VEGF antagonists. The KDR nucleic acid sequence

can be transfected into cells for analysis of function in the absence of Flt-1. The KDR protein is also useful for x-ray structure analysis in the presence or absence of ligand and/or inhibitors. The present invention addresses and meets these needs by disclosing an isolated nucleic acid  
5 fragment which expresses a form of human KDR which is shown by computer modeling to be predictive of higher activity and functionality than the previously disclosed KDR.

#### SUMMARY OF THE INVENTION

10 The present invention relates to an isolated nucleic acid molecule (polynucleotide) which encodes a novel human receptor type tyrosine kinase gene, KDR. This specification discloses a novel, optimized DNA molecule which encodes, KDR, a receptor tyrosine kinase expressed on human endothelial cells.

15 The present invention also relates to biologically active fragments or mutants of SEQ ID NO:1 which encodes mRNA expressing a novel human receptor type tyrosine kinase gene, KDR. Any such biologically active fragment and/or mutant will encode either a protein or protein fragment comprising at least an intracellular or extracellular  
20 kinase domain similar to that of the human KDR protein as set forth in SEQ ID NO:2. Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions, deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of  
25 diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists for KDR function.

The isolated nucleic acid molecule of the present invention may include a deoxyribonucleic acid molecule (DNA), such as genomic DNA and complementary DNA (cDNA), which may be single (coding or  
30 noncoding strand) or double stranded, as well as synthetic DNA, such as a synthesized, single stranded polynucleotide. The isolated nucleic acid molecule of the present invention may also include a ribonucleic acid molecule (RNA).

35 The present invention also relates to recombinant vectors and recombinant hosts, both prokaryotic and eukaryotic, which contain

the substantially purified nucleic acid molecules disclosed throughout this specification.

5 The present invention also relates to subcellular membrane fractions of the recombinant host cells (both prokaryotic and eukaryotic as well as both stably and transiently transformed cells) comprising the nucleic acids of the present invention. These subcellular membrane fractions will comprise either wild-type or human mutant forms of KDR at levels substantially above wild-type levels and hence will be useful in various assays described throughout this specification.

10 A preferred aspect of the present invention is disclosed in Figure 1A and Figure 1B and SEQ ID NO:1, a human cDNA encoding a novel receptor type tyrosine kinase gene, KDR.

15 The present invention also relates to a substantially purified form of the receptor type tyrosine kinase gene, KDR which is disclosed in Figure 2 and as set forth in SEQ ID NO:2.

20 The present invention also relates to biologically active fragments and/or mutants of the KDR protein as initially set forth as SEQ ID NO:2, including but not necessarily limited to amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations such that these mutations provide for proteins or protein fragments of diagnostic, therapeutic or prophylactic use and would be useful for screening for agonists and/or antagonists for KDR function.

25 A preferred aspect of the present invention is disclosed in Figure 2 and is set forth as SEQ ID NO:2, the amino acid sequence of the novel receptor type tyrosine kinase gene, KDR.

The present invention also relates to polyclonal and monoclonal antibodies raised in response to either the human form of KDR disclosed herein, or a biologically active fragment thereof.

30 The present invention also relates to isolated nucleic acid molecules which are fusion constructions expressing fusion proteins useful in assays to identify compounds which modulate wild-type human KDR activity. A preferred aspect of this portion of the invention includes, but is not limited to, glutathione S-transferase (GST)-KDR fusion constructs. These fusion constructs include, but are not limited to, either the intracellular tyrosine kinase domain of human KDR as an

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in-frame fusion at the carboxy terminus of the GST gene or the extracellular ligand binding domain fused to an immunoglobulin gene by methods known to one of ordinary skill in the art. Soluble recombinant GST-kinase domain fusion proteins may be expressed in  
5 various expression systems, including *Spodoptera frugiperda* (Sf21) insect cells (Invitrogen) using a baculovirus expression vector (pAcG2T, Pharmingen).

The present invention also relates to isolated nucleic acid molecules which encode human KDR protein fragments comprising a  
10 portion of the intracellular KDR domain. The protein fragments are useful in assays to identify compounds which modulate wild-type human KDR activity. A preferred aspect of this portion of the invention includes, but is not limited to, a nucleic acid construction which encodes the intracellular portion of human KDR, from about amino acid 780 - 795  
15 to about amino acid 1175 - 1386.

Therefore, the present invention relates to isolated nucleic acid molecules which encode human KDR protein fragments comprising a portion of the extracellular KDR domain. These isolated nucleic acid proteins may or may not include nucleotide sequences  
20 which also encode the transmembrane domain of human KDR. These KDR extracellular and/or KDR extracellular-transmembrane domain protein fragments will be useful in screening for compounds which inhibit VEGF binding as well as utilizing these isolated nucleic acids as gene therapy vehicles to inhibit VEGF-mediated mitogenic activity.  
25 Expression of either a soluble version of KDR (extracellular) or membrane bound form (extracellular-transmembrane) will inhibit *in vivo* VEGF/KDR mediated angiogenesis.

Therefore, the present invention relates to methods of expressing the receptor type tyrosine kinase gene, KDR, and biological  
30 equivalents disclosed herein, assays employing these receptor type tyrosine kinase genes, cells expressing these receptor type tyrosine kinase genes, and compounds identified through the use of these receptor type tyrosine kinase genes and expressed human KDR protein, including one or more modulators of the human KDR-dependent kinase  
35 either through direct contact with the kinase domain of human KDR or a compound which prevents binding of VEGF to human KDR, or

appropriate dimerization of the KDR receptor antagonizing transduction of the normal intracellular signals associated with VEGF-induced angiogenesis.

5 The present invention also relates to gene therapy applications, especially for nucleic acid fragments which encode soluble extracellular protein fragments of human KDR. It is disclosed herein that such methods will be useful especially in the treatment of various tumors as well as diabetic retinopathy.

10 It is an object of the present invention to provide an isolated nucleic acid molecule which encodes a novel form of human KDR, or human KDR fragments and KDR mutants which are derivatives of SEQ ID NO:2 and preferably retain Val at position 848, and especially preferable is retention of Val at position 848, Glu at position 498, Ala at position 772, Arg at position 787, Lys at position 835 and Ser at position 15 1347. Any such polynucleotide includes but is not necessarily limited to nucleotide substitutions, deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and would be useful for 20 screening for agonists and/or antagonists for KDR function.

It is a further object of the present invention to provide the human KDR proteins or protein fragments encoded by the nucleic acid molecules referred to in the preceding paragraph.

25 It is also an object of the present invention to provide biologically active fragments or mutants of human KDR which comprise an intracellular kinase domain similar to that of the human KDR protein as set forth in SEQ ID NO:2, preferably retaining Val at position 848, and especially preferable is retention of Val at position 848, Glu at position 498, Ala at position 772, Arg at position 787, Lys at position 835 30 and Ser at position 1347.

It is a further object of the present invention to provide recombinant vectors and recombinant host cells which comprise a nucleic acid sequence encoding human KDR or a biological equivalent thereof.

It is an object of the present invention to provide a substantially purified form of the receptor type tyrosine kinase gene, KDR, as set forth in SEQ ID NO:2.

It is an object of the present invention to provide for  
5 biologically active fragments and/or mutants of the KDR protein, such as set forth in SEQ ID NO:2, including but not necessarily limited to amino acid substitutions, deletions, additions, amino terminal truncations and carboxy-terminal truncations such that these mutations provide for proteins or protein fragments of diagnostic,  
10 therapeutic or prophylactic use.

It is also an object of the present invention to provide for KDR-based in-frame fusion constructions, methods of expressing the receptor type tyrosine kinase gene, KDR, and biological equivalents disclosed herein, related assays, recombinant cells expressing these  
15 receptor type tyrosine kinase genes, and agonistic and/or antagonistic compounds identified through the use of these receptor type tyrosine kinase genes and expressed human KDR protein.

As used herein, "VEGF" or "VEFG-A" refers to vascular endothelial growth factor.

20 As used herein, "KDR" or "FLK-1" refers to kinase insert domain-containing receptor.

As used herein, "FLT-1" refers to fms-like tyrosine kinase receptor.

25 As used herein, the term "mammalian host" refers to any mammal, including a human being.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A and Figure 1B show the nucleotide sequence which encodes human KDR, as set forth in SEQ ID NO:1.

30 Figure 2 shows the amino acid sequence of human KDR, as also set forth in SEQ ID NO:2. Underlined amino acid residues represent differences in comparison to a previously disclosed form of human KDR.

Figure 3A shows the ATP binding domain from the KDR V848E mutant homology model with bound AMP-PCP. The side chain of  
35 E848 is in contact the adenine from AMP-PCP. The gamma phosphate

of AMP-PCP is not visible. The protein carbon alpha trace is shown in pipes, the AMP-PCP in sticks and the E848 side chain in space filling. The N-terminal lobe is colored blue (or alternatively labeled with light circles) with the exception of the glycine rich flap which is colored green  
5 (or alternatively labeled as a lined region). The C-terminal lobe is colored red (or alternatively labeled with dark circles).

Figure 3B shows ATP binding domain from the KDR homology model with bound AMP-PCP. The side chain of V848 forms hydrophobic contacts with the adenine from AMP-PCP. The gamma  
10 phosphate of AMP-PCP is not visible. The protein carbon alpha trace is shown in pipes, the AMP-PCP in sticks and the V848 side chain in space filling. The N-terminal lobe is colored blue (or alternatively labeled with light circles) with the exception of the glycine rich flap which is colored green (or alternatively labeled as a lined region). The C-terminal lobe is  
15 colored red (or alternatively labeled with dark circles).

Figure 4A and 4B show that purified GST-KDR<sub>cyt</sub>E848 was unable to autophosphorylate in the presence of 1-mM ATP wherein 12 ng of GST-KDR<sub>cyt</sub>V848 in the presence of 1 mM ATP resulted in autophosphorylation (Figure 4A) and that both both 120 ng of GST-  
20 KDR<sub>cyt</sub>E848 and 12 ng of GST-KDR<sub>cyt</sub>V848 react with anti-KDR antibody (Figure 4B).

#### DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to isolated nucleic acid and  
25 protein forms which represent human KDR. This specification discloses a DNA molecule encoding human KDR, a receptor tyrosine kinase expressed on human endothelial cells. The receptor is activated by vascular endothelial growth factor (VEGF) and mediates a mitogenic signal. This activation and subsequent mitogenesis leads to an  
30 angiogenic response *in vivo*. The nucleic acid molecule disclosed in the specification as SEQ ID NO:1 encodes a human KDR protein (SEQ ID NO:2) which results in six amino acid differences from the published sequence (Terman et al., 1992, *Biochem. Biophys. Res. Commun.* 187: 1579-1586, Terman et al., International PCT application number WO  
35 92/14748, International application number PCT/US92/01300). These changes are position 498 (Ala to Glu), 772 (Thr to Ala), 787 (Gly to Arg),

835 (Asn to Lys), 848 (Glu to Val), and 1347 (Thr to Ser). These six amino acid changes affect the activity of the receptor. Val 848 is conserved throughout most of the tyrosine kinase family and appears to be important for the binding of ATP and presumably ATP competitive inhibitors to the KDR receptor kinase as inferred by computer modeling. A change to Glu at this position results in a non-functional kinase as a consequence of impaired ATP binding. The other changes may also cause activity differences.

The present invention also relates to either biologically active fragments or mutants of SEQ ID NO:1 which encodes mRNA expressing a novel human receptor type tyrosine kinase gene, KDR. Any such biologically active fragment and/or mutant will encode a protein or protein fragment comprising at least an intracellular kinase domain similar to that of the human KDR protein as set forth in SEQ ID NO:2 and preferably retain Val at position 848. It is also envisioned that other intracellular-based KDR domains will result in a soluble protein fragment which mimics wild-type intracellular domain structure and function. Any such protein fragment may be a fusion protein, such as the exemplified GST-KDR fusion, or may be solely comprised of the KDR intracellular domain, with increasing deletions in from the COOH-terminal region. It is especially preferable that the following amino acids be retained, if this domain encompasses the respective protein or protein fragment: Val at position 848, Glu at position 498, Ala at position 772, Arg at position 787, Lys at position 835 and Ser at position 1347. Therefore, any such polynucleotide includes but is not necessarily limited to nucleotide substitutions, deletions, additions, amino-terminal truncations and carboxy-terminal truncations such that these mutations encode mRNA which express a protein or protein fragment of diagnostic, therapeutic or prophylactic use and is useful for the identification of modulators of KDR receptor activity.

The isolated nucleic acid molecule of the present invention may include a deoxyribonucleic acid molecule (DNA), such as genomic DNA and complementary DNA (cDNA), which may be single (coding or noncoding strand) or double stranded, as well as synthetic DNA, such as a synthesized, single stranded polynucleotide. The isolated nucleic

acid molecule of the present invention may also include a ribonucleic acid molecule (RNA).

It is known that DNA sequences coding for a peptide may be altered so as to code for a peptide having properties that are different  
5 than those of the naturally occurring peptide. Methods of altering the DNA sequences include but are not limited to site directed mutagenesis. Examples of altered properties include but are not limited to changes in the affinity of an enzyme for a substrate or a receptor for a ligand.

As used herein, "purified" and "isolated" are utilized  
10 interchangeably to stand for the proposition that the nucleic acid, protein, or respective fragment thereof in question has been substantially removed from its *in vivo* environment so that it may be manipulated by the skilled artisan, such as but not limited to nucleotide sequencing, restriction digestion, site-directed mutagenesis, and  
15 subcloning into expression vectors for a nucleic acid fragment as well as obtaining the protein or protein fragment in pure quantities so as to afford the opportunity to generate polyclonal antibodies, monoclonal antibodies, amino acid sequencing, and peptide digestion. Therefore, the nucleic acids claimed herein may be present in whole cells or in cell  
20 lysates or in a partially purified or substantially purified form. A nucleic acid is considered substantially purified when it is purified away from environmental contaminants. Thus, a nucleic acid sequence isolated from cells is considered to be substantially purified when purified from cellular components by standard methods while a  
25 chemically synthesized nucleic acid sequence is considered to be substantially purified when purified from its chemical precursors.

The present invention also relates to recombinant vectors and recombinant hosts, both prokaryotic and eukaryotic, which contain the substantially purified nucleic acid molecules disclosed throughout  
30 this specification.

The present invention also relates to subcellular membrane fractions of the recombinant host cells (both prokaryotic and eukaryotic as well as both stably and transiently transformed cells) comprising the nucleic acids of the present invention. These subcellular membrane  
35 fractions will comprise wild-type or human mutant forms of KDR at

levels substantially above wild-type levels and hence will be useful in various assays described throughout this specification.

A preferred aspect of the present invention is disclosed in Figure 1A and Figure 1B and SEQ ID NO:1, a human cDNA encoding a novel receptor type tyrosine kinase gene, KDR, disclosed as follows:

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ATGGAGAGCAAGGTGCTGCTGGCCGTCGCCCTGTGGCTCTGCGTGGAGACCCGGGCGCCTCTGTGGGT
TTGCCTAGTGTCTTCTTGGATCTGCCCAGGCTCAGCATACAAAAGACATACTTACAATTAAGGCTAAT
ACAACCTCTTCAAATTACTTGCAGGGGACAGAGGGACTTGGACTGGCTTTGGCCCAATAATCAGAGTGGC
10 AGTGAGCAAAGGGTGGAGGTGACTGAGTGCAGCGATGGCCTCTTCTGTAAGACACTCACAATTCCAAAA
GTGATCGGAAATGACACTGGAGCCTACAAGTGCTTCTACCGGGAACCTGACTTGGCCTCGGTCATTAT
GTCTATGTTCAAGATTACAGATCTCCATTTATTGCTTCTGTAGTGACCAACATGGAGTCGTGTACATT
ACTGAGAACAAAAACAAACTGTGGTGATTCCATGTCTCGGGTCCATTTCAAATCTCAACGTGTCACTT
TGTGCAAGATACCCAGAAAAGAGATTTGTTCCCTGATGGTAACAGAATTTCCCTGGGACAGCAAGAAGGGC
15 TTTACTATTCCCAGCTACATGATCAGCTATGCTGGCATGGTCTTCTGTGAAGCAAAAATTAATGATGAA
AGTTACCAGTCTATTATGTACATAGTTGTCTGTTGATGGGTATAGGATTTATGATGTGGTTCTGAGTCCG
TCTCATGGAATTGAACATCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAAGTGAACATAAAT
GTGGGGATTGACTTCAACTGGGAATACCCCTTCTTCGAAGCATCAGCATAAGAACTTGTAAACCGAGAC
CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTGAGCACCTTAACATATAGATGGTGTAACCCGG
20 AGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC
AGGGTCCATGAAAAACCTTTTGTGCTTTTGGAAAGTGGCATGGAATCTCTGGTGGAAAGCCACGGTGGGG
GAGCGTGTGAGAATCCCTGCGAAGTACCTTGGTTACCCACCCCGAGAAATAAAATGGTATAAAAATGGA
ATACCCCTTGAGTCCAATCACACAATTAAGCGGGGCATGTACTGACGATTATGGAAGTGAGTGAAAGA
GACACAGGAAATTACACTGTATCCTTACCAATCCCATTTCAAAGGAGAAGCAGAGCCATGTGGTCTCT
25 CTGGTTGTGATGTCTCCACCCAGATTGGTGAGAAATCTTAATCTCTCCTGTGGATTCTTACCAGTAC
GGCACCACTCAAACGCTGACATGTACGGTCTATGCCATTCCTCCCGCATCACATCCACTGGATTGG
CAGTTGGAGGAAGAGTGCGCCAACGAGCCAGCCAAGCTGTCTCAGTGACAAACCCATACCCTTGTGAA
GAATGGAGAAGTGTGGAGGACTTCCAGGGAGGAAATAAAATGAAGTTAATAAAAATCAATTTGCTCTA
ATTGAAGGAAAAAACAACTGTAAGTACCCTTGTATCCAAGCGGCAAATGTGTGAGCTTTGTACAAA
30 TGTGAAGCGGTCAACAAAGTCGGGAGAGGAGAGAGGGTGATCTCCTTCCACGTGACCAGGGGTCCTGAA
ATTACTTTGCAACCTGACATGCAGCCCAGTGCAGGAGAGCGTGTCTTTGTGGTGCAGTGCAGACAGA
TCTACGTTTGTGAGAACCTCACATGGTACCAAGCTTGGCCCCACAGCCTCTGCCAATCCATGTGGGAGAGTTG
CCCACACCTGTTTGAAGAAGTGGATACTCTTTGGAAATTGAATGCCACCATTGTCTCTGATAGCACA
AATGACATTTTGTATCATGGAGCTTAAGAATGCATCCTTGCAGGACCAAGGAGACTATGTCTGCCTTGCT
35 CAAGACAGGAAGACCAAGAAAAGACATTGCGTGGTCAGGCAGCTCACAGTCCTAGAGCGTGTGGCACC
ACGATCACAGGAAACCTGGAGAATCAGACGACAAGTATTGGGGAAAGCATCGAAGTCTCATGCACGGCA
TCTGGGAATCCCCCTCCACAGATCATGTGGTTTAAAGATAATGAGACCCCTTGTAGAAGACTCAGGCATT
GTATTGAAGGATGGGAACCGGAACCTCACTATCCGAGAGTGAGGAAGGAGGACGAAGGCCTCTACACC
TGCCAGGCATGCAGTGTCTTGGCTGTGCAAAAGTGGAGGCATTTTTCATAATAGAAGGTGCCAGGAA
40 AAGACGAACTTGGAAATCATTTATTCTAGTAGGCACGGCGGTGATTGCCATGTTCTTCTGGCTACTTCTT
GTCATCATCCTACGGACCGTTAAGCGGGCCAATGGAGGGGAAGTGAAGACAGGCTACTTGTCCATCGTC
ATGGATCCAGATGAACTCCCATTTGGATGAACATTGTGAACGACTGCCTTATGATGCCAGCAAATGGGAA
TTCCCCAGAGACCGGCTGAAGCTAGGTAAGCCTCTTGGCCGTGGTGCCTTTGGCCAAGTGATTGAAGCA
GATGCCTTTGGAATTGACAAGACAGCAACTTGCAGGACAGTAGCAGTCAAAATGTTGAAAGAAGGAGCA
45 ACACACAGTGAGCATCGAGCTCTCATGTCTGAACTCAAGATCCTCATTCATATTGGTCAACCATCTCAAT
GTGGTCAACCTTCTAGGTGCCGTGTACCAAGCCAGGAGGGCCACTCATGGTGATTGTGGAATTTCTGCAA
TTTGGAAACCTGTCCACTTACCTGAGGAGCAAGAGAAATGAATTTGTCCCTACAAGACCAAGGGGCA
CGATTCCGTCAAGGGAAGACTACGTTGGAGCAATCCCTGTGGATCTGAAACGGCGCTTGGACAGCATC
ACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTTGTGGAGGAGAAGTCCCTCAGTGATGTAGAAGAAGAG
50 GAAGCTCCTGAAGATCTGTATAAGGACTTCTTGACCTTGGAGCATCTCATCTGTTACAGCTTCCAAGTG
GCTAAGGGCATGGAGTTCTTGGCATCGCGAAAGTGATCCACAGGGACCTGGCGGCACGAAATATCCTC
TTATCGGAGAAGAAGCTGGTTAAATCTGTGACTTTGGCTTGGCCCGGGATATTTATAAAGATCCAGAT
TATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGATGGCCCCAGAAACAATTTTGTACAGAGTG
TACACAATCCAGAGTGACGTCTGGTCTTTTGGTGTGCTGTGGGAAATATTTTCCCTTAGGTGCTTCT
55 CCATATCCTGGGGTAAAGATTGATGAAGAATTTTGTAGGCGATTGAAAGAAGGAAGTGAATGAGGGCC

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CCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGGCACGGGGAGCCCAGTCAGAGA  
 CCCACGTTTTTCAGAGTTGGTGGAACATTTGGGAAATCTCTTGCAAGCTAATGCTCAGCAGGATGGCAAA  
 GACTACATTGTTCTTCCGATATCAGAGACTTTGAGCATGGAAGAGGATTCTGGACTCTCTCTGCCTACC  
 5 TCACCTGTTTCTCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCATTATGACAACACAGCAGGA  
 ATCAGTCAGTATCTGCAGAACAGTAAGCGAAAAGAGCCGGCCTGTGAGTGTAAAAACATTTGAAGATATC  
 CCGTTAGAAGAACCAGAAGTAAAAGTAATCCAGATGACAACCAGACGGACAGTGGTATGGTTCTTGCC  
 TCAGAAGAGCTGAAAACATTTGGAAGACAGAACCAAATTTATCTCCATCTTTTGGTGGAAATGGTGGCCAGC  
 AAAAGCAGGGAGTCTGTGGCATCTGAAGGCTCAAACCAGACAAGCGGCTACCAGTCCGGATATCACTCC  
 10 GATGACACAGACACCACCGTGTACTCCAGTGAGGAAGCAGAACTTTTAAAGCTGATAGAGATTGGAGTG  
 CAAACCGGTAGCACAGCCCAGATTCTCCAGCCTGACTCGGGGACCACACTGAGCTCTCCTCTGTTTAA  
 (SEQ ID NO:1).

The present invention also relates to a substantially purified  
 form of the receptor type tyrosine kinase gene which comprises the KDR  
 15 amino acid sequence disclosed in Figure 2 and as set forth in SEQ ID  
 NO:2, which includes Glu at position 498, Ala at position 772, Arg at  
 position 787, Lys at position 835, Val at position 848 and Ser at position  
 1347, disclosed as follows:

20 MESKVLALLVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLWLWPNNQSG  
 SEQRVEVTECSDFLCKTLTIKVIIGNDTGAYKCFYRETDLASVIYVYVQDYRSPFIASVSDQHGVVYI  
 TENKNKTVVIPCGLGISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFEAKINDE  
 SYQSIMYIVVVVGRIYDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEYPSSKHQHKLVNRD  
 25 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVG  
 ERVRIPAKYLGYPPPEIKWYKNGIPLSNHTIKAGHVLTIMEVSRDTGNYTVILTNPISKEKQSHVVS  
 LVVYVPPQIGEKSLISPVDSYQYGTQTTLCTVYAIPPPHHIHWWQLEEECANEPSQAVSVTNPYPCPE  
 EWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPE  
 ITLQPDQMPTQESVSLWCTADRSTFENLTWYKLGQPLPIHVGEPLTPVCKNLDTLWKLNATMFSNST  
 30 NDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRLTVLERVAPTITGNLENQTTSIGESIEVSCSTA  
 SGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIIRVRKEDEGLYTCQACSVLGC AKVEAFFIIEGAQE  
 KTNLEIIILVGTAVIAMFFWLLLVIILRTVTKRANGGELKTGYLSIVMDPDELPLDEHCELRPYDASKWE  
 FPRDRLKLGKPLGRGAFQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLN  
 VVNLGACTKPGGPLMVIVEFCKFGNLSTYLSKRNEFVYPYKTKGARFRQKDYVGAIPVDLKRRLDSI  
 35 TSSQSSASSGFVEEKSLSVDEEEEAPELDYKDFLTLEHLICYSFQVAKGMEFLASRKC IHRDLAARNIL  
 LSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGAS  
 PYPGVKIDEEFCRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDQK  
 DYIVLPISSETLSMEEDSGLSLPTSPVSCMEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDI  
 PLEEPEVKVIPDDNQTDSGMVLASEELKTLEDRTKLSPSFSGMVPSKSRRESVASEGNSQTSQYQSGYHS  
 40 DDTDTTVYSSEEAEELLKLEIGVQTGSTAQILQPDGTTLSPPV (SEQ ID NO:2).

The present invention also relates to biologically active  
 fragments and/or mutants of the KDR protein as initially set forth as  
 SEQ ID NO:2, including but not necessarily limited to amino acid  
 substitutions, deletions, additions, amino terminal truncations and  
 carboxy-terminal truncations such that these mutations provide for  
 45 proteins or protein fragments of diagnostic, therapeutic or prophylactic  
 use and would be useful for screening for agonists and/or antagonists  
 for KDR function.



A preferred aspect of the present invention is disclosed in Figure 2 and is set forth as SEQ ID NO:2, the amino acid sequence of the novel receptor type tyrosine kinase gene, KDR.

5 The present invention also relates to isolated nucleic acid molecules which are fusion constructions useful in assays to identify compounds which modulate wild-type human KDR activity. A preferred aspect of this portion of the invention includes, but is not limited to, GST-KDR fusion constructs. These fusion constructs comprise the intracellular tyrosine kinase domain of human KDR as an in-frame  
10 fusion at the carboxy terminus of the GST gene. Soluble recombinant GST-kinase domain fusion proteins may be expressed in various expression systems, including *Spodoptera frugiperda* (Sf21) insect cells (Invitrogen) using a baculovirus expression vector (pAcG2T, Pharmingen).

15 The present invention relates to isolated nucleic acid molecules which encode soluble portions of the KDR intracellular or extracellular domain. Especially preferred are nucleic acid molecules which encode a COOH-terminal deletion KDR protein fragment useful in assays to identify compounds which modulate wild-type human KDR  
20 activity. Any such nucleic acid will encode a KDR protein fragment which mimics KDR wild-type activity within the respective domain, such as the kinase domain of human KDR. These expressed soluble protein fragments may or may not contain a portion of the amino-terminal region of human KDR or of a heterologous sequence. These  
25 nucleic acids may be expressed in any of a number of expression systems available to the artisan. Any such intracellular-based KDR construction of the present invention may be utilized in gene therapy applications, such as acting as an soluble agonist or antagonist of kinase activity normally associated with wild type, membrane  
30 associated kinase activity.

Therefore, the present invention relates to isolated nucleic acid molecules which encode human KDR protein fragments comprising a portion of the intracellular KDR domain. The protein fragments are useful in assays to identify compounds which modulate  
35 wild-type human KDR activity. A preferred aspect of this portion of the invention includes, but is not limited to, a nucleic acid construction

which encodes the intracellular portion of human KDR, from about amino acid 780 - 795 to about amino acid 1175 - 1386. The data exemplified in Example Section 3 show that COOH terminal deletions of the soluble intracellular portion of KDR exhibit kinase activity.

5           The present invention also relates to isolated nucleic acid molecules which encode human KDR protein fragments comprising a portion of the extracellular KDR domain. These isolated nucleic acid proteins may or may not include nucleotide sequences which also encode the transmembrane domain of human KDR. These KDR  
10 extracellular and/or KDR extracellular-transmembrane domain protein fragments will be useful in screening for compounds which inhibit VEGF binding as well as utilizing these isolated nucleic acids as gene therapy vehicles to inhibit VEGF-mediated mitogenic activity. Expression of wither a soluble version of KDR (extracellular) or  
15 membrane bound form (extracellular-transmembrane) will inhibit VEGF/KDR mediated angiogenesis. A preferred aspect of this portion of the invention includes, but is not limited to, an isolated nucleic acid molecule which encodes at least six of the IG-like extracellular domains from the amino-terminal end of KDR. Such a protein fragment would  
20 comprise at least from about the initiating methionine to about amino acid 644 of human KDR (SEQ ID NO:2). Another preferred aspect of this portion of the invention includes, but is not limited to, an isolated nucleic acid molecule which encodes the all seven IG-like extracellular domains from the amino-terminal end of KDR. Such a protein fragment  
25 would comprise at least from about the initiating methionine to about amino acid 763. An additional preferred embodiment includes but is not limited to an extracellular-transmembrane construct which encodes about the initial 785 - 795 amino acids of KDR as set forth in SEQ ID NO:2, and especially preferred is an isolated nucleic acid molecule  
30 construction which encodes the amino terminal portion of KDR with a truncation at about amino acid 791 as set forth in SEQ ID NO:2.

Therefore, the present invention relates to methods of expressing the receptor type tyrosine kinase gene, KDR, and biological equivalents disclosed herein, assays employing these receptor type  
35 tyrosine kinase genes, cells expressing these receptor type tyrosine kinase genes, and agonistic and/or antagonistic compounds identified

through the use of these receptor type tyrosine kinase genes and expressed human KDR protein, including, but not limited to, one or more modulators of the human KDR-dependent kinase either through direct contact with the kinase domain of human KDR or a compound  
5 which prevents binding of VEGF to human KDR, or either prevents or promotes receptor dimerization and/or activation thereby either inducing or antagonizing transduction of the normal intracellular signals associated with VEGF-induced angiogenesis

As used herein, a "biologically active equivalent" or  
10 "functional derivative" of a wild-type human KDR possesses a biological activity that is substantially similar to the biological activity of the wild type human KDR. The term "functional derivative" is intended to include the "fragments," "mutants," "variants," "degenerate variants," "analogs" and "homologues" or to "chemical derivatives" of the wild type  
15 human KDR protein. The term "fragment" is meant to refer to any polypeptide subset of wild-type human KDR. The term "mutant" is meant to refer to a molecule that may be substantially similar to the wild-type form but possesses distinguishing biological characteristics. Such altered characteristics include but are in no way limited to altered  
20 substrate binding, altered substrate affinity and altered sensitivity to chemical compounds affecting biological activity of the human KDR or human KDR functional derivative. The term "variant" is meant to refer to a molecule substantially similar in structure and function to either the entire wild-type protein or to a fragment thereof. A molecule is  
25 "substantially similar" to a wild-type human KDR-like protein if both molecules have substantially similar structures or if both molecules possess similar biological activity. Therefore, if the two molecules possess substantially similar activity, they are considered to be variants even if the structure of one of the molecules is not found in the other or  
30 even if the two amino acid sequences are not identical. The term "analog" refers to a molecule substantially similar in function to either the full-length human KDR protein or to a biologically active fragment thereof.

Any of a variety of procedures may be used to clone human  
35 KDR. These methods include, but are not limited to, (1) a RACE PCR cloning technique (Frohman, et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:

8998-9002). 5' and/or 3' RACE may be performed to generate a full-length cDNA sequence. This strategy involves using gene-specific oligonucleotide primers for PCR amplification of human KDR cDNA. These gene-specific primers are designed through identification of an expressed sequence tag (EST) nucleotide sequence which has been identified by searching any number of publicly available nucleic acid and protein databases; (2) direct functional expression of the human KDR cDNA following the construction of a human KDR-containing cDNA library in an appropriate expression vector system; (3) screening a human KDR-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a labeled degenerate oligonucleotide probe designed from the amino acid sequence of the human KDR protein; and (4) screening a human KDR-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a partial cDNA encoding the human KDR protein. This partial cDNA is obtained by the specific PCR amplification of human KDR DNA fragments through the design of degenerate oligonucleotide primers from the amino acid sequence known for other kinases which are related to the human KDR protein; (5) screening a human KDR-containing cDNA library constructed in a bacteriophage or plasmid shuttle vector with a partial cDNA encoding the human KDR protein. This strategy may also involve using gene-specific oligonucleotide primers for PCR amplification of human KDR cDNA identified as an EST as described above; or (6) designing 5' and 3' gene specific oligonucleotides using SEQ ID NO: 1 as a template so that either the full-length cDNA may be generated by known RACE techniques, or a portion of the coding region may be generated by these same known RACE techniques to generate and isolate a portion of the coding region to use as a probe to screen one of numerous types of cDNA and/or genomic libraries in order to isolate a full-length version of the nucleotide sequence encoding human KDR.

It is readily apparent to those skilled in the art that other types of libraries, as well as libraries constructed from other cell types or species types, may be useful for isolating a human KDR-encoding DNA or a human KDR homologue. Other types of libraries include, but are not limited to, cDNA libraries derived from other cells or cell lines other than human cells or tissue such as murine cells, rodent cells or any

other such vertebrate host which may contain human KDR-encoding DNA. Additionally a human KDR gene and homologues may be isolated by oligonucleotide- or polynucleotide-based hybridization screening of a vertebrate genomic library, including but not limited to, a murine  
5 genomic library, a rodent genomic library, as well as concomitant human genomic DNA libraries.

It is readily apparent to those skilled in the art that suitable cDNA libraries may be prepared from cells or cell lines which have KDR activity. The selection of cells or cell lines for use in preparing a cDNA  
10 library to isolate a cDNA encoding human KDR may be done by first measuring cell-associated KDR activity using any known assay available for such a purpose.

Preparation of cDNA libraries can be performed by standard techniques well known in the art. Well known cDNA library  
15 construction techniques can be found for example, in Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory, Cold Spring Harbor, New York. Complementary DNA libraries may also be obtained from numerous commercial sources, including but not limited to Clontech Laboratories, Inc. and Stratagene.

It is also readily apparent to those skilled in the art that DNA encoding human KDR may also be isolated from a suitable  
20 genomic DNA library. Construction of genomic DNA libraries can be performed by standard techniques well known in the art. Well known genomic DNA library construction techniques can be found in  
25 Sambrook, et al., *supra*.

In order to clone the human KDR gene by one of the preferred methods, the amino acid sequence or DNA sequence of human KDR or a homologous protein may be necessary. To accomplish this, the KDR protein or a homologous protein may be purified and  
30 partial amino acid sequence determined by automated sequenators. It is not necessary to determine the entire amino acid sequence, but the linear sequence of two regions of 6 to 8 amino acids can be determined for the PCR amplification of a partial human KDR DNA fragment. Once suitable amino acid sequences have been identified, the DNA  
35 sequences capable of encoding them are synthesized. Because the genetic code is degenerate, more than one codon may be used to encode a

particular amino acid, and therefore, the amino acid sequence can be encoded by any of a set of similar DNA oligonucleotides. Only one member of the set will be identical to the human KDR sequence but others in the set will be capable of hybridizing to human KDR DNA even in the presence of DNA oligonucleotides with mismatches. The mismatched DNA oligonucleotides may still sufficiently hybridize to the human KDR DNA to permit identification and isolation of human KDR encoding DNA. Alternatively, the nucleotide sequence of a region of an expressed sequence may be identified by searching one or more available genomic databases. Gene-specific primers may be used to perform PCR amplification of a cDNA of interest from either a cDNA library or a population of cDNAs. As noted above, the appropriate nucleotide sequence for use in a PCR-based method may be obtained from SEQ ID NO: 1, either for the purpose of isolating overlapping 5' and 3' RACE products for generation of a full-length sequence coding for human KDR, or to isolate a portion of the nucleotide sequence coding for human KDR for use as a probe to screen one or more cDNA- or genomic-based libraries to isolate a full-length sequence encoding human KDR or human KDR-like proteins.

In an exemplified method, the human KDR full-length cDNA of the present invention was generated by screening a human umbilical vein endothelial cell (HUVEC) lambda phage cDNA library with a KDR-specific 576 base pair DNA probe prepared by using primers KDR-A: 5'-GGAATTCCATCCAAGCGGCAAATGTGTC-3' (SEQ ID NO:3) and KDR-B: 5'-GGAATTCCGAGTCTTCTACAAGGGTCTC-3' (SEQ ID NO:4). Lambda phage clones containing unique inserts were isolated through three rounds of replating and then characterized. The 3' 110 base pairs not represented in any of the isolated clones were cloned by PCR from the same library as above using the primers KDR-C: 5'-TTATGACAACACAGCAGG-3' (SEQ ID NO:5) and KDR-D: 5'-TTGGATCCTCGAGTTGGGGTGTGGATGC-3' (SEQ ID NO:6). Overlapping clones were used to generate a full-length KDR gene into plasmid vector pGEM7Z. The gene contained an XhoI site at the 5' end which was changed to a BamHI site by first cutting with XhoI, then forming a blunt end with DNA polymerase and ligating an oligonucleotide BamHI linker and finally cloned as a BamHI/BamHI

fragment back into pGEM7Z. The gene was sequenced on an ABI Prism automatic sequencer model number 377. In addition, the cytoplasmic domain of KDR which contains tyrosine kinase activity was cloned separately as a GST gene fusion into a baculovirus expression vector to  
5 characterize tyrosine kinase activity.

A variety of mammalian expression vectors may be used to express recombinant human KDR in mammalian cells. Expression vectors are defined herein as DNA sequences that are required for the transcription of cloned DNA and the translation of their mRNAs in an  
10 appropriate host. Such vectors can be used to express eukaryotic DNA in a variety of hosts such as bacteria, blue green algae, plant cells, insect cells and animal cells. Specifically designed vectors allow the shuttling of DNA between hosts such as bacteria-yeast or bacteria-animal cells. An appropriately constructed expression vector should  
15 contain: an origin of replication for autonomous replication in host cells, selectable markers, a limited number of useful restriction enzyme sites, a potential for high copy number, and active promoters. A promoter is defined as a DNA sequence that directs RNA polymerase to bind to DNA and initiate RNA synthesis. A strong promoter is one  
20 which causes mRNAs to be initiated at high frequency. Expression vectors may include, but are not limited to, cloning vectors, modified cloning vectors, specifically designed plasmids or viruses.

Commercially available mammalian expression vectors which may be suitable for recombinant human KDR expression, include  
25 but are not limited to, pcDNA3.1 (Invitrogen), pLITMUS28, pLITMUS29, pLITMUS38 and pLITMUS39 (New England Biolabs), pcDNA1, pcDNA1amp (Invitrogen), pcDNA3 (Invitrogen), pMC1neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2-neo (ATCC 37593) pBPV-1(8-2) (ATCC 37110), pDBPV-MMTneo(342-12) (ATCC 37224),  
30 pRSVgpt (ATCC 37199), pRSVneo (ATCC 37198), pSV2-dhfr (ATCC 37146), pUCtag (ATCC 37460), and  $\lambda$ ZD35 (ATCC 37565).

A variety of bacterial expression vectors may be used to express recombinant human KDR in bacterial cells. Commercially available bacterial expression vectors which may be suitable for  
35 recombinant human KDR expression include, but are not limited to

pCR2.1 (Invitrogen), pET11a (Novagen), lambda gt11 (Invitrogen), and pKK223-3 (Pharmacia).

5 A variety of fungal cell expression vectors may be used to express recombinant human KDR in fungal cells. Commercially available fungal cell expression vectors which may be suitable for recombinant human KDR expression include but are not limited to pYES2 (Invitrogen) and *Pichia* expression vector (Invitrogen).

10 A variety of insect cell expression vectors may be used to express recombinant receptor in insect cells. Commercially available insect cell expression vectors which may be suitable for recombinant expression of human KDR include but are not limited to pBlueBacIII and pBlueBacHis2 (Invitrogen), and pAcG2T (Pharmingen).

15 An expression vector containing DNA encoding a human KDR-like protein may be used for expression of human KDR in a recombinant host cell. Recombinant host cells may be prokaryotic or eukaryotic, including but not limited to bacteria such as *E. coli*, fungal cells such as yeast, mammalian cells including but not limited to cell lines of human, bovine, porcine, monkey and rodent origin, and insect cells including but not limited to *Drosophila*- and silkworm-derived cell  
20 lines. Cell lines derived from mammalian species which may be suitable and which are commercially available, include but are not limited to, L cells L-M(TK-) (ATCC CCL 1.3), L cells L-M (ATCC CCL 1.2), Saos-2 (ATCC HTB-85), 293 (ATCC CRL 1573), Raji (ATCC CCL 86), CV-1 (ATCC CCL 70), COS-1 (ATCC CRL 1650), COS-7 (ATCC CRL 1651), CHO-K1 (ATCC CCL 61), 3T3 (ATCC CCL 92), NIH/3T3 (ATCC CRL 1658), HeLa (ATCC CCL 2), C127I (ATCC CRL 1616), BS-C-1 (ATCC CCL 26), MRC-5 (ATCC CCL 171) and CPAE (ATCC CCL 209).

30 The expression vector may be introduced into host cells via any one of a number of techniques including but not limited to transformation, transfection, protoplast fusion, and electroporation. The expression vector-containing cells are individually analyzed to determine whether they produce human KDR protein. Identification of human KDR expressing cells may be done by several means, including but not limited to immunological reactivity with anti-human KDR  
35 antibodies, labeled ligand binding and the presence of host cell-associated human KDR activity.



The cloned human KDR cDNA obtained through the methods described above may be recombinantly expressed by molecular cloning into an expression vector (such as pcDNA3.1, pCR2.1, pBlueBacHis2 and pLITMUS28) containing a suitable promoter and other appropriate transcription regulatory elements, and transferred into prokaryotic or eukaryotic host cells to produce recombinant human KDR. Techniques for such manipulations can be found described in Sambrook, et al., *supra*, are discussed at length in the Example section and are well known and easily available to the artisan of ordinary skill in the art.

Expression of human KDR DNA may also be performed using *in vitro* produced synthetic mRNA. Synthetic mRNA can be efficiently translated in various cell-free systems, including but not limited to wheat germ extracts and reticulocyte extracts, as well as efficiently translated in cell based systems, including but not limited to microinjection into frog oocytes, with microinjection into frog oocytes being preferred.

To determine the human KDR cDNA sequence(s) that yields optimal levels of human KDR, cDNA molecules including but not limited to the following can be constructed: a cDNA fragment containing the full-length open reading frame for human KDR as well as various constructs containing portions of the cDNA encoding only specific domains of the protein or rearranged domains of the protein. All constructs can be designed to contain none, all or portions of the 5' and/or 3' untranslated region of a human KDR cDNA. The expression levels and activity of human KDR can be determined following the introduction, both singly and in combination, of these constructs into appropriate host cells. Following determination of the human KDR cDNA cassette yielding optimal expression in transient assays, this KDR cDNA construct is transferred to a variety of expression vectors (including recombinant viruses), including but not limited to those for mammalian cells, plant cells, insect cells, oocytes, bacteria, and yeast cells.

Levels of human KDR in host cells is quantified by a variety of techniques including, but not limited to, immunoaffinity and/or ligand affinity techniques. KDR-specific affinity beads or KDR-specific

antibodies are used to isolate <sup>35</sup>S-methionine labeled or unlabelled KDR. Labeled KDR protein is analyzed by SDS-PAGE. Unlabelled KDR protein is detected by Western blotting, ELISA or RIA assays employing either KDR protein specific antibodies and/or antiphosphotyrosine antibodies.

5                   Following expression of KDR in a host cell, KDR protein may be recovered to provide KDR protein in active form. Several KDR protein purification procedures are available and suitable for use. Recombinant KDR protein may be purified from cell lysates and extracts, or from conditioned culture medium, by various combinations  
10 of, or individual application of salt fractionation, ion exchange chromatography, size exclusion chromatography, hydroxylapatite adsorption chromatography and hydrophobic interaction chromatography.

                  In addition, recombinant KDR protein can be separated  
15 from other cellular proteins by use of an immunoaffinity column made with monoclonal or polyclonal antibodies specific for full-length KDR protein, or polypeptide fragments of KDR protein. Additionally, polyclonal or monoclonal antibodies may be raised against a synthetic peptide (usually from about 9 to about 25 amino acids in length) from a  
20 portion of the protein as disclosed in SEQ ID NO:2. Monospecific antibodies to human KDR are purified from mammalian antisera containing antibodies reactive against human KDR or are prepared as monoclonal antibodies reactive with human KDR using the technique of Kohler and Milstein (1975, *Nature* 256: 495-497). Monospecific antibody  
25 as used herein is defined as a single antibody species or multiple antibody species with homogenous binding characteristics for human KDR. Homogenous binding as used herein refers to the ability of the antibody species to bind to a specific antigen or epitope, such as those associated with human KDR, as described above. Human KDR-specific  
30 antibodies are raised by immunizing animals such as mice, rats, guinea pigs, rabbits, goats, horses and the like, with an appropriate concentration of human KDR protein or a synthetic peptide generated from a portion of human KDR with or without an immune adjuvant.

                  Preimmune serum is collected prior to the first  
35 immunization. Each animal receives between about 0.1 µg and about 1000 µg of human KDR protein associated with an acceptable immune

adjuvant. Such acceptable adjuvants include, but are not limited to, Freund's complete, Freund's incomplete, alum-precipitate, water in oil emulsion containing *Corynebacterium parvum* and tRNA. The initial immunization consists of human KDR protein or peptide fragment  
5 thereof in, preferably, Freund's complete adjuvant at multiple sites either subcutaneously (SC), intraperitoneally (IP) or both. Each animal is bled at regular intervals, preferably weekly, to determine antibody titer. The animals may or may not receive booster injections following the initial immunization. Those animals receiving booster injections  
10 are generally given an equal amount of human KDR in Freund's incomplete adjuvant by the same route. Booster injections are given at about three week intervals until maximal titers are obtained. At about 7 days after each booster immunization or about weekly after a single immunization, the animals are bled, the serum collected, and aliquots  
15 are stored at about -20°C.

Monoclonal antibodies (mAb) reactive with human KDR are prepared by immunizing inbred mice, preferably Balb/c, with human KDR protein. The mice are immunized by the IP or SC route with about 1 µg to about 100 µg, preferably about 10 µg, of human KDR  
20 protein in about 0.5 ml buffer or saline incorporated in an equal volume of an acceptable adjuvant, as discussed above. Freund's complete adjuvant is preferred. The mice receive an initial immunization on day 0 and are rested for about 3 to about 30 weeks. Immunized mice are given one or more booster immunizations of about 1 to about 100 µg of  
25 human KDR in a buffer solution such as phosphate buffered saline by the intravenous (IV) route. Lymphocytes, from antibody positive mice, preferably splenic lymphocytes, are obtained by removing spleens from immunized mice by standard procedures known in the art. Hybridoma cells are produced by mixing the splenic lymphocytes with an  
30 appropriate fusion partner, preferably myeloma cells, under conditions which will allow the formation of stable hybridomas. Fusion partners may include, but are not limited to: mouse myelomas P3/NS1/Ag 4-1; MPC-11; S-194 and Sp 2/0, with Sp 2/0 being preferred. The antibody producing cells and myeloma cells are fused in polyethylene glycol,  
35 about 1000 mol. wt., at concentrations from about 30% to about 50%. Fused hybridoma cells are selected by growth in hypoxanthine,

thymidine and aminopterin supplemented Dulbecco's Modified Eagles Medium (DMEM) by procedures known in the art. Supernatant fluids are collected from growth positive wells on about days 14, 18, and 21 and are screened for antibody production by an immunoassay such as solid  
5 phase immunoradioassay (SPIRA) using human KDR as the antigen. The culture fluids are also tested in the Ouchterlony precipitation assay to determine the isotype of the mAb. Hybridoma cells from antibody positive wells are cloned by a technique such as the soft agar technique of MacPherson, 1973, *Soft Agar Techniques*, in *Tissue Culture Methods and Applications*, Kruse and Paterson, Eds., Academic Press.  
10

Monoclonal antibodies are produced *in vivo* by injection of pristine primed Balb/c mice, approximately 0.5 ml per mouse, with about  $2 \times 10^6$  to about  $6 \times 10^6$  hybridoma cells about 4 days after priming. Ascites fluid is collected at approximately 8-12 days after cell transfer  
15 and the monoclonal antibodies are purified by techniques known in the art.

*In vitro* production of anti-human KDR mAb is carried out by growing the hybridoma in DMEM containing about 2% fetal calf serum to obtain sufficient quantities of the specific mAb. The mAb are  
20 purified by techniques known in the art.

Antibody titers of ascites or hybridoma culture fluids are determined by various serological or immunological assays which include, but are not limited to, precipitation, passive agglutination, enzyme-linked immunosorbent antibody (ELISA) technique and  
25 radioimmunoassay (RIA) techniques. Similar assays are used to detect the presence of human KDR in body fluids or tissue and cell extracts.

It is readily apparent to those skilled in the art that the above described methods for producing monospecific antibodies may be utilized to produce antibodies specific for human KDR peptide  
30 fragments, or full-length human KDR.

Human KDR antibody affinity columns are made, for example, by adding the antibodies to Affigel-10 (Biorad), a gel support which is pre-activated with N-hydroxysuccinimide esters such that the antibodies form covalent linkages with the agarose gel bead support.  
35 The antibodies are then coupled to the gel via amide bonds with the spacer arm. The remaining activated esters are then quenched with 1M

ethanolamine HCl (pH 8). The column is washed with water followed by 0.23 M glycine HCl (pH 2.6) to remove any non-conjugated antibody or extraneous protein. The column is then equilibrated in phosphate buffered saline (pH 7.3) and the cell culture supernatants or cell extracts  
5 containing full-length human KDR or human KDR protein fragments are slowly passed through the column. The column is then washed with phosphate buffered saline until the optical density (A<sub>280</sub>) falls to background, then the protein is eluted with 0.23 M glycine-HCl (pH 2.6). The purified human KDR protein is then dialyzed against phosphate  
10 buffered saline.

The human KDR protein of the present invention is suitable for use in an assay procedure for the identification of compounds which modulate KDR activity. A KDR-containing fusion construct, such as a GST-KDR fusion as discussed within this specification, is useful to  
15 measure KDR activity. Kinase activity is, for example, measured by incorporation of radiolabeled phosphate into polyglutamic acid, tyrosine, 4:1 (pEY) substrate. The phosphorylated pEY product is trapped onto a filter membrane and the incorporation of radiolabeled phosphate quantified by scintillation counting. Soluble recombinant GST-kinase  
20 domain fusion proteins are expressed in Sf21 insect cells (Invitrogen) using a baculovirus expression vector (pAcG2T, Pharmingen). A lysis buffer is 50 mM Tris, pH 7.4, 0.5 M NaCl, 5 mM DTT, 1 mM EDTA, 0.5% Triton X-100, 10% glycerol, 10 µg/ml of each leupeptin, pepstatin and aprotinin and 1 mM phenylmethylsulfonyl fluoride (all Sigma). A wash  
25 buffer is 50 mM Tris, pH 7.4, 0.5 M NaCl, 5 mM DTT, 1 mM EDTA, 0.05% Triton X-100, 10% glycerol, 10 µg/ml of each leupeptin, pepstatin and aprotinin and 1 mM phenylmethylsulfonyl fluoride. A dialysis buffer is 50 mM Tris, pH 7.4, 0.5 M NaCl, 5 mM DTT, 1 mM EDTA, 0.05% Triton X-100, 50% glycerol, 10 µg/ml of each leupeptin, pepstatin  
30 and aprotinin and 1 mM phenylmethylsulfonyl fluoride. A 10X reaction buffer is 200 mM Tris, pH 7.4, 1.0 M NaCl, 50 mM MnCl<sub>2</sub>, 10 mM DTT and 5 mg/ml bovine serum albumin (Sigma). An enzyme dilution buffer is 50 mM Tris, pH 7.4, 0.1 M NaCl, 1 mM DTT, 10% glycerol, 100 mg/ml BSA. A 10X substrate solution would be 750 µg/ml poly(glutamic acid,  
35 tyrosine; 4:1) (Sigma); stop solution is 30% trichloroacetic acid, 0.2 M sodium pyrophosphate (both Fisher) and wash solution is 15%

trichloroacetic acid, 0.2 M sodium pyrophosphate. The filter plates are Millipore #MAFC NOB, GF/C glass fiber 96 well plates.

First, Sf21 cells are infected with recombinant virus at a multiplicity of infection of 5 virus particles/cell and grown at 27 °C for 48 hours. All subsequent steps are performed at 4 °C. Infected cells are harvested by centrifugation at 1000 X g and lysed at 4 °C for 30 minutes with 1/10 volume of lysis buffer followed by centrifugation at 100,000Xg for 1 hour. The supernatant is then passed over a glutathione-Sepharose column (Pharmacia) equilibrated in lysis buffer and washed with 5 volumes of the same buffer followed by 5 volumes of wash buffer. Recombinant GST-KDR protein is eluted with wash buffer/10 mM reduced glutathione (Sigma) and dialyzed against dialysis buffer.

The KDR assay comprises the following steps:

1. Add 5 µl of inhibitor or control to the assay in 50% DMSO;
2. Add 35 µl of reaction mix containing 5 µl of 10 X reaction buffer, 5 µl 25 mM ATP/10 µCi [<sup>33</sup>P]ATP (Amersham), and 5 µl 10 X substrate;
3. Start the reaction by the addition of 10 µl of KDR (25 nM) in enzyme dilution buffer;
4. Mix and incubate at room temperature (~22 °C) for 15 minutes;
5. Stop by the addition of 50 µl stop solution;
6. Incubate for 15 minutes at 4 °C;
7. Transfer a 90 µl aliquot to filter plate;
8. Aspirate and wash 3 times with 100 µl of wash solution;
9. Add 30 µl of scintillation cocktail, seal plate and count in a Wallac Microbeta scintillation counter.

Modulating KDR includes the inhibition or activation of the kinase which affects the mitogenic function of VEGF. Compounds which modulate KDR include agonists and antagonists.

Therefore, the human KDR protein of the present invention may be obtained from both native and recombinant sources (as a full-length protein, biologically active protein fragment, or fusion construction) for use in an assay procedure to identify human KDR modulators. In general, an assay procedure to identify human KDR modulators will contain the intracellular domain of human KDR, and a

test compound or sample which contains a putative KDR kinase agonist or antagonist. The test compounds or samples may be tested directly on, for example, purified KDR, KDR kinase or a GST-KDR kinase fusion, subcellular fractions of KDR-producing cells whether native or  
5 recombinant, whole cells expressing human KDR whether native or recombinant, intracellular KDR protein fragments and respective deletion fragments, and/or extracellular intracellular KDR protein fragments and respective deletion fragments. The test compound or sample may be added to KDR in the presence or absence of a known  
10 human KDR substrate. The modulating activity of the test compound or sample may be determined by, for example, analyzing the ability of the test compound or sample to bind to the KDR intracellular domain, activate the protein, inhibit the protein, inhibit or enhance the binding of other compounds to human KDR, modifying VEGF receptor regulation,  
15 or modifying kinase activity.

Therefore, the present invention also relates to subcellular membrane fractions of the recombinant host cells (both prokaryotic and eukaryotic as well as both stably and transiently transformed cells) comprising the nucleic acids of the present invention. These  
20 subcellular membrane fractions will comprise human KDR at levels substantially above wild-type levels and hence will be useful in various assays described throughout this specification.

The identification of modulators of human KDR will be useful in treating various disease states. For example, vascular growth  
25 in or near the retina leads to visual degeneration culminating in blindness. VEGF accounts for most of the angiogenic activity produced in or near the retina in diabetic retinopathy. Ocular VEGF mRNA and protein are elevated by conditions such as retinal vein occlusion in primates and decreased  $pO_2$  levels in mice that lead to  
30 neovascularization. Expression of VEGF is also significantly increased in hypoxic regions of animal and human tumors adjacent to areas of necrosis. VEGF contributes to tumor growth *in vivo* by promoting angiogenesis through its paracrine vascular endothelial cell chemotactic and mitogenic activities. Inhibition of KDR is implicated in  
35 pathological neoangiogenesis, and compounds which inhibit the mitogenic activity of VEGF via inhibition of KDR will be useful in the

treatment of diseases in which neoangiogenesis is part of the overall pathology, such as diabetic retinal vascularization, various forms of cancer and inflammation which demonstrate high levels of gene and protein expression. Examples of such cancers include cancers of the  
5 brain, breast, genitourinary tract, lymphatic system, stomach, intestines including colon, pancreas, prostate, larynx and lung. These include histiocytic lymphoma, lung adenocarcinoma, glioblastoma and small cell lung cancers. Examples of inflammation include  
10 rheumatoid arthritis, psoriasis, contact dermatitis and hypersensitivity reactions.

The present invention also relates to gene transfer of a DNA vector and concomitant *in vivo* expression of an extracellular, soluble form of human KDR, preferably comprising from about amino acid 1 to from about amino acid 644 (to encompass the initial six IG-like  
15 extracellular domains) to about amino acid 763 (to encompass all seven IG-like extracellular domains) of human KDR as set forth in SEQ ID NO:2. Such a gene therapy vehicle will express this soluble form of human KDR, which binds VEGF or a VEGF homologue in and around the localized site of the disorder. The formation of a sKDR/VEGF  
20 complex will inhibit binding of VEGF to the KDR and FLT-1 tyrosine kinase receptors spanning the vascular endothelial cell membrane, thus preventing initiation of the signal transduction stimulating angiogenesis. In addition, expression of sKDR may also impart a therapeutic effect by binding to membrane associated VEGF receptors.  
25 VEGF receptors are thought to be dimerized by binding dimeric VEGF ligand which in turn allows the receptor intracellular tyrosine kinase domains to transphosphorylate each other generating phosphorylated tyrosine residues that facilitate the subsequent binding and activation of downstream signal transduction proteins. Soluble KDR will be able to  
30 form heterodimers with full-length VEGF receptors that, because the sKDR forms are devoid of an intracellular tyrosine kinase region, prevent receptor tyrosine kinase domain transphosphorylation, the initiation of signal transduction and thus VEGF-induced mitogenesis and angiogenesis in a dominant negative manner. The skilled artisan  
35 will be able to generate various gene therapy constructs which express various regions of the extracellular domain of KDR for administration to



the patient. While the patient may be any mammalian host, the preferable treatment is directed toward humans. Any such construct will express a KDR fragment which effectively inhibits mitogenic activity associated with VEGF/KDR associations on human endothelial cells. It is preferred in the present invention that this region comprise an isolated nucleic acid molecule which encodes from about amino acid 1 to about amino acid 644 and/or from about amino acid 1 to about amino acid 763 as set forth in SEQ ID NO:2.

Another preferred embodiment of the present invention is a nucleic acid molecule which encodes an extracellular-transmembrane KDR protein fragment which is also useful in gene therapy applications as described in the previous paragraph. It is preferred that any such DNA molecule comprise a DNA sequence from which encodes from about amino acid 1 to about amino acid about the initial 785 - 795 amino acids of KDR as set forth in SEQ ID NO:2, and especially preferred is an isolated nucleic acid molecule construction which encodes the amino terminal portion of KDR with a truncation at about amino acid 791 as set forth in SEQ ID NO:2.

One preferred gene therapy application for the human KDR gene and protein of the present invention relates to promoting inhibition of solid tumor angiogenesis and metastasis by utilizing the disclosed gene therapy methodology. A second preferred gene therapy application for the human KDR gene and protein of the present invention relates to promoting inhibition of diabetic retinopathy, as described elsewhere within this specification. The transferred sKDR nucleic acid is expressed within the region of interest subsequent to gene transfer such that expressed sKDR binds to VEGF to prevent binding of VEGF to the KDR and FLT-1 tyrosine kinase receptors, antagonizing transduction of the normal intracellular signals associated with vascular endothelial cell-induced tumor angiogenesis and diabetic retinopathy.

The present invention is also directed to methods for screening for compounds which modulate the expression of DNA or RNA encoding a human KDR protein. Compounds which modulate these activities may be DNA, RNA, peptides, proteins, or non-proteinaceous organic molecules. Compounds may modulate by increasing or attenuating the expression of DNA or RNA encoding

human KDR, or the function of human KDR. Compounds that modulate the expression of DNA or RNA encoding human KDR or the biological function thereof may be detected by a variety of assays. The assay may be a simple "yes/no" assay to determine whether there is a  
5 change in expression or function. The assay may be made quantitative by comparing the expression or function of a test sample with the levels of expression or function in a standard sample. Kits containing human KDR, antibodies to human KDR, or modified human KDR may be prepared by known methods for such uses.

10 The DNA molecules, RNA molecules, recombinant protein and antibodies of the present invention may be used to screen and measure levels of human KDR. The recombinant proteins, DNA molecules, RNA molecules and antibodies lend themselves to the formulation of kits suitable for the detection and typing of human KDR.  
15 Such a kit would comprise a compartmentalized carrier suitable to hold in close confinement at least one container. The carrier would further comprise reagents such as recombinant KDR or anti-KDR antibodies suitable for detecting human KDR. The carrier may also contain a means for detection such as labeled antigen or enzyme substrates or the  
20 like.

Pharmaceutically useful compositions comprising modulators of human KDR may be formulated according to known methods such as by the admixture of a pharmaceutically acceptable carrier. Examples of such carriers and methods of formulation may be  
25 found in Remington's Pharmaceutical Sciences. To form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of the protein, DNA, RNA, modified human KDR, or either KDR agonists or antagonists including tyrosine kinase activators or inhibitors.

30 Therapeutic or diagnostic compositions of the invention are administered to an individual in amounts sufficient to treat or diagnose disorders. The effective amount may vary according to a variety of factors such as the individual's condition, weight, sex and age. Other factors include the mode of administration.

The pharmaceutical compositions may be provided to the individual by a variety of routes such as subcutaneous, topical, oral and intramuscular.

5 The term "chemical derivative" describes a molecule that contains additional chemical moieties which are not normally a part of the base molecule. Such moieties may improve the solubility, half-life, absorption, etc. of the base molecule. Alternatively the moieties may attenuate undesirable side effects of the base molecule or decrease the toxicity of the base molecule. Examples of such moieties are described  
10 in a variety of texts, such as Remington's Pharmaceutical Sciences.

Compounds identified according to the methods disclosed herein may be used alone at appropriate dosages. Alternatively, co-administration or sequential administration of other agents may be desirable.

15 The present invention also has the objective of providing suitable topical, oral, systemic and parenteral pharmaceutical formulations for use in the novel methods of treatment of the present invention. The compositions containing compounds identified according to this invention as the active ingredient can be administered  
20 in a wide variety of therapeutic dosage forms in conventional vehicles for administration. For example, the compounds can be administered in such oral dosage forms as tablets, capsules (each including timed release and sustained release formulations), pills, powders, granules, elixirs, tinctures, solutions, suspensions, syrups and emulsions, or by  
25 injection. Likewise, they may also be administered in intravenous (both bolus and infusion), intraperitoneal, subcutaneous, topical with or without occlusion, or intramuscular form, all using forms well known to those of ordinary skill in the pharmaceutical arts.

Advantageously, compounds of the present invention may  
30 be administered in a single daily dose, or the total daily dosage may be administered in divided doses of two, three or four times daily. Furthermore, compounds for the present invention can be administered in intranasal form via topical use of suitable intranasal vehicles, or via transdermal routes, using those forms of transdermal skin patches well  
35 known to those of ordinary skill in that art. To be administered in the form of a transdermal delivery system, the dosage administration will,

of course, be continuous rather than intermittent throughout the dosage regimen.

For combination treatment with more than one active agent, where the active agents are in separate dosage formulations, the active agents can be administered concurrently, or they each can be administered at separately staggered times.

The dosage regimen utilizing the compounds of the present invention is selected in accordance with a variety of factors including type, species, age, weight, sex and medical condition of the patient; the severity of the condition to be treated; the route of administration; the renal, hepatic and cardiovascular function of the patient; and the particular compound thereof employed. A physician or veterinarian of ordinary skill can readily determine and prescribe the effective amount of the drug required to prevent, counter or arrest the progress of the condition. Optimal precision in achieving concentrations of drug within the range that yields efficacy without toxicity requires a regimen based on the kinetics of the drug's availability to target sites. This involves a consideration of the distribution, equilibrium, and elimination of a drug.

The following examples are provided to illustrate the present invention without, however, limiting the same hereto.

#### EXAMPLE 1

##### Isolation of a cDNA Encoding Human KDR

*Materials* - A human umbilical vein endothelial cell lambda phage cDNA library was purchased from Clontech (Cat. # HL1070b). DNA modification and restriction enzymes were purchased from Promega. Plasmid pGEM7Z was purchased from Promega (Cat. # P2251). Taq polymerase was from Perkin Elmer Cetus (part number N801-0055). BamHI linkers were purchased from New England Biolabs (Cat. # 1071). [ $\alpha$ -<sup>32</sup>P] dATP was purchased from Amersham (Cat. # PB 10204). Rediprime was also purchased from Amersham (Cat. # RPN 1633). The baculovirus expression vector pAcG2T was purchased from Pharmingen (Cat. # 21414P).

The PCR primers used are as follows:

KDR-A 5'-GGAATTCCATCCAAGCGGCAAATGTGTC-3' (SEQ ID NO:3);

KDR-B 5'-GGAATTCCGAGTCTTCTACAAGGGTCTC-3' (SEQ ID NO:4)

5 KDR-C 5'-TTATGACAACACAGCAGG-3' (SEQ ID NO:5); and,

KDR-D 5'-TTGGATCCTCGAGTTGGGGTGTGGATGC-3' (SEQ ID NO:6).

*Methods: Gene Cloning* - The KDR cDNA was isolated by probing a human umbilical vein endothelial cell lambda phage cDNA library from Clonetech with a KDR-specific 576 base pair DNA probe. The probe was prepared by PCR using primers KDR-A/KDR-B and Taq polymerase, then labeled to a specific activity of  $1 \times 10^7$  cpm/ng by random priming. Phage were plated at about 50,000 plaques/plate and hybridization was done by standard protocols. A total of  $1 \times 10^6$  phage were screened. Lambda phage clones containing unique inserts were isolated through three rounds of replating and then characterized. The 3' 110 base pairs not represented in any of the isolated clones were cloned by PCR from the same library as above using the primers KDR-C and KDR-D. Overlapping clones were used to generate a full-length KDR gene by restriction enzyme digestion, isolation of the individual gene fragments and ligation (restriction enzymes and ligase were from Promega) into pGEM7Z. The gene contained an XhoI site at the 5' end which was changed to a BamHI site by first cutting with XhoI, then forming a blunt end with DNA polymerase and ligating an oligonucleotide BamHI linker and finally cloned as a BamHI/BamHI fragment back into pGEM7Z. The gene was sequenced on an ABI Prism automatic sequencer model number 377. The cDNA sequence of human KDR is shown in Figure 1A and 1B. The deduced amino acid sequence of human KDR is shown in Figure 2.

30

## EXAMPLE 2

### Construction of GST/KDR-1

The cytoplasmic domain of KDR which contains tyrosine kinase activity was cloned separately as a glutathione S-transferase (GST) gene fusion into a baculovirus expression vector to characterize

35

tyrosine kinase activity. To construct this GST fusion, a Kpn I cloning site was introduced into the KDR gene by changing the codons encoding residues Gly 800 (GGG to GGC) and Leu 802 (TTG to CTG) and the existing BamHI site was removed by changing the codon encoding Asp 807 (GAT to GAC); these changes are silent and do not change the amino acid sequence of the receptor. A new BamHI site was introduced to form an in frame fusion with the carboxyl terminus of GST and KDR at Ala 792. The GST and KDR BamHI-digested fragments were ligated to generate the in frame GST/KDR fusion. Active GST-KDR tyrosine kinase protein is produced in insect cells.

### EXAMPLE 3

#### Construction Of KDR Core Kinase Domain

The kinase domain of KDR was cloned using the preexisting BamHI site at the 5' end of the kinase domain and introducing a stop codon followed by a SalI site at the 3' end of the kinase domain (Tyr 1175 TAC changed to TAA). KDR DNA was used as a template in a PCR reaction with primers KDR-E (5'-GGATCCAGATGAACTCCCATTTG-3' [SEQ ID NO:7]) and KDR-F (5'-GTCGACTTAGTCTTTGCCATCCTGCTGAGC-3' [SEQ ID NO:8]). The resulting KDR core kinase BamHI/Sal I fragment was cloned into pBlueBacHis2B, this creates an inframe fusion of the methionine initiator codon and the poly histidine sequence of the vector with the KDR kinase domain. This vector, pBBH-KDR-1, also provides an enterokinase recognition site to remove the His tag polypeptide by proteolysis. The KDR core kinase protein was expressed in insect cells and purified on a nickel chelating column. The purified KDR core kinase was active in the kinase assay described herein.

### EXAMPLE 4

#### Molecular Modeling of Human KDR

The cytoplasmic domain of the VEGF receptor was aligned by hand to the sequence of FGFR1 as taken from the published crystal structure (Mohammadi, M., Schlessinger, J. and Hubbard, S.R., 1996,

*Cell* 86: 577). The sequences are ~60% identical in this alignment. An  
homology model of KDR kinase was then built in Quanta (version 4.1p)  
by copying the coordinates from the FGFR1/AMP-PCP crystal structure.  
The kinase insert region (residues 933-1006 in KDR) was not included in  
5 the model since there was no unique conformation for this region in the  
crystal structure. The homology model was then minimized using  
CHARMM within Quanta constraining the protein backbone and  
allowing the side chains to move freely.

The change of amino acid residue 848 from the published  
10 Glu to Val in SEQ ID NO:2 is found in the glycine-rich flap, which forms  
part of the ATP binding pocket. The highly conserved Val is found to  
form hydrophobic contacts to ATP in other kinases, and appears to be  
positioned to form these same contacts in KDR. A charged Glu in this  
position is not likely to make proper contact with ATP. This is shown by  
15 computer modeling in Figure 3A and Figure 3B. Figure 3A shows the  
ATP binding domain from the KDR V848E mutant homology model with  
bound AMP-PCP. The side chain of E848 is in contact the adenine from  
AMP-PCP. The gamma phosphate of AMP-PCP is not visible. The  
protein carbon alpha trace is shown in pipes, the AMP-PCP in sticks  
20 and the E848 side chain in space filling. The N-terminal lobe is colored  
blue (or alternatively labeled with light circles) with the exception of the  
glycine rich flap which is colored green (or alternatively labeled as a  
lined region). The C-terminal lobe is colored red (or alternatively labeled  
with dark circles). Figure 3B shows ATP binding domain from the KDR  
25 homology model with bound AMP-PCP. The side chain of V848 forms  
hydrophobic contacts with the adenine from AMP-PCP. The gamma  
phosphate of AMP-PCP is not visible. The protein carbon alpha trace is  
shown in pipes, the AMP-PCP in sticks and the V848 side chain in space  
filling. The N-terminal lobe is colored blue (or alternatively labeled with  
30 light circles) with the exception of the glycine rich flap which is colored  
green (or alternatively labeled as a lined region). The C-terminal lobe is  
colored red (or alternatively labeled with dark circles).

## EXAMPLE 5

Tyrosine Phosphorylation of KDR<sub>cyt</sub> Mutants

Purified KDR<sub>cyt</sub>E848 and KDR<sub>cyt</sub>V848 were incubated with  
5 at concentrations of 12 ng or 120 ng, respectively, or without 1 mM ATP  
at 37 °C for 10 min. The reaction was stopped by the addition of an equal  
volume of 2X SDS-PAGE sample buffer and boiled for 5 min. Reaction  
products were separated by 7.5%/SDS-PAGE and analyzed by Western  
10 blot probed with the antiphosphotyrosine antibody PY20 (Transduction  
Laboratories; Figure 4A), or an anti-KDR antibody (Santa Cruz  
Biotechnology; Figure 4B) visualized using the ECL detection kit and  
quantified by scanning with a densitometer (Molecular Dynamics).  
Figure 4A shows that purified GST-KDR<sub>cyt</sub>E848 was unable to  
autophosphorylate in the presence of 1-mM ATP wherein 12 ng of GST-  
15 KDR<sub>cyt</sub>V848 in the presence of 1 mM ATP resulted in  
autophosphorylation. Figure 4B shows a signal against anti-KDR  
antibody for 120 ng GST-KDR<sub>cyt</sub>E848 and 12 ng of GST-KDR<sub>cyt</sub>V848.



## SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- (i) APPLICANTS: Merck & Co., Inc.
- 10 (ii) TITLE OF INVENTION: HUMAN RECEPTOR TYROSINE KINASE, KDR
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Merck & Co., Inc.
- (B) STREET: P.O. Box 2000
- (C) CITY: Rahway
- (D) STATE: NJ
- (E) COUNTRY: US
- 20 (F) ZIP: 07065-0907
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- 30 (B) FILING DATE:
- (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Hand, J. Mark
- 35 (B) REGISTRATION NUMBER: 36,545
- (C) REFERENCE/DOCKET NUMBER: 19963PV
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 732/594-3905
- 40 (B) TELEFAX: 732/594-4720
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- 45 (A) LENGTH: 4071 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|    |  |      |
|----|--|------|
|    | ATGGAGAGCA AGGTGCTGCT GGCCGTCGCC CTGTGGCTCT GCGTGGAGAC CCGGGCCGCC  | 60   |
| 5  | TCTGTGGGTT TGCCTAGTGT TTCTCTTGAT CTGCCCAGGC TCAGCATACA AAAAGACATA  | 120  |
|    | CTTACAATTA AGGCTAATAC AACTCTTCAA ATTACTTGCA GGGGACAGAG GGA CTGAGC  | 180  |
| 10 | TGGCTTTGGC CCAATAATCA GAGTGGCAGT GAGCAAAGGG TGGAGGTGAC TGAGTGCAGC  | 240  |
|    | GATGGCCTCT TCTGTAAGAC ACTCACAATT CAAAAGTGA TCGGAAATGA CACTGGAGCC   | 300  |
|    | TACAAGTGCT TCTACCGGA AACTGACTTG GCCTCGGTCA TTTATGTCTA TGTTCAGAT    | 360  |
| 15 | TACAGATCTC CATTTATTGC TTCTGTTAGT GACCAACATG GAGTCGTGTA CATTACTGAG  | 420  |
|    | AACAAAAACA AAAGTGTGGT GATTCCATGT CTCGGGTCCA TTCAAATCT CAACGTGTCA   | 480  |
| 20 | CTTTGTGCAA GATACCCAGA AAAGAGATTT GTTCCTGATG GTAACAGAAT TTCTGGGAC   | 540  |
|    | AGCAAGAAGG GCTTTACTAT TCCCAGCTAC ATGATCAGCT ATGCTGGCAT GGTCTTCTGT  | 600  |
|    | GAAGCAAAAA TTAATGATGA AAGTTACCAG TCTATTATGT ACATAGTTGT CGTTGTAGGG  | 660  |
| 25 | TATAGGATTT ATGATGTGGT TCTGAGTCCG TCTCATGGAA TTGAACTATC TGTGAGAA    | 720  |
|    | AAGCTTGTCT TAAATTGTAC AGCAAGAAGT GAAGTAAATG TGGGGATTGA CTTCACTGG   | 780  |
| 30 | GAATACCCTT CTTCGAAGCA TCAGCATAAG AAAGTGTGTA ACCGAGACCT AAAAACCAG   | 840  |
|    | TCTGGGAGTG AGATGAAGAA ATTTTGTAGC ACCTTAACTA TAGATGGTGT AACCCGAGT   | 900  |
|    | GACCAAGGAT TGTACACCTG TGCAGCATCC AGTGGGCTGA TGACCAAGAA GAACAGCACA  | 960  |
| 35 | TTTGTGAGGG TCCATGAAAA ACCTTTTGTG GCTTTTGGAA GTGGCATGGA ATCTCTGGTG  | 1020 |
|    | GAAGCCACGG TGGGGGAGCG TGTGAGAATC CCTGCGAAGT ACCTTGTTA CCCACCCCA    | 1080 |
| 40 | GAAATAAAAT GGTATAAAAA TGGAATACCC CTTGAGTCCA ATCACACAAT TAAAGCGGGG  | 1140 |
|    | CATGTACTGA CGATTATGGA AGTGAGTGAA AGAGACACAG GAAATTACAC TGTATCCTT   | 1200 |
|    | ACCAATCCCA TTTCAAAGGA GAAGCAGAGC CATGTGGTCT CTCTGGTTGT GTATGTCCCA  | 1260 |
| 45 | CCCCAGATTG GTGAGAAATC TCTAATCTCT CCTGTGGATT CCTACCAGTA CGGCACCACT  | 1320 |
|    | CAAACGCTGA CATGTACGGT CTATGCCATT CCTCCCCGC ATCACATCCA CTGGTATTGG   | 1380 |
| 50 | CAGTTGGAGG AAGAGTGC GC CAACGAGCCC AGCCAAGCTG TCTCAGTGAC AAACCCATAC | 1440 |
|    | CCTTGTGAAG AATGGAGAAG TGTGGAGGAC TTCCAGGGAG GAAATAAAAT TGAAGTTAAT  | 1500 |
|    | AAAAATCAAT TTGCTCTAAT TGAAGGAAAA AACAAACTG TAAGTACCCT TGTATCCAA    | 1560 |
| 55 | GCGGCAAATG TGTGAGCTTT GTACAAATGT GAAGCGGTCA ACAAAGTCGG GAGAGGAGAG  | 1620 |
|    | AGGGTGATCT CCTTCCACGT GACCAGGGGT CCTGAAATTA CTTTGCAACC TGACATGCAG  | 1680 |

|    |            |            |            |            |            |             |      |
|----|------------|------------|------------|------------|------------|-------------|------|
|    | CCCACTGAGC | AGGAGAGCGT | GTCTTTGTGG | TGCACTGCAG | ACAGATCTAC | GTTTGAGAAC  | 1740 |
|    | CTCACATGGT | ACAAGCTTGG | CCCACAGCCT | CTGCCAATCC | ATGTGGGAGA | GTTGCCCCACA | 1800 |
| 5  | CCTGTTTGCA | AGAACTTGGA | TACTCTTTGG | AAATTGAATG | CCACCATGTT | CTCTAATAGC  | 1860 |
|    | ACAAATGACA | TTTTGATCAT | GGAGCTTAAG | AATGCATCCT | TGCAGGACCA | AGGAGACTAT  | 1920 |
| 10 | GTCTGCCTTG | CTCAAGACAG | GAAGACCAAG | AAAAGACATT | GCGTGGTCAG | GCAGCTCACA  | 1980 |
|    | GTCCTAGAGC | GTGTGGCACC | CACGATCACA | GGAAACCTGG | AGAATCAGAC | GACAAGTATT  | 2040 |
|    | GGGGAAAGCA | TCGAAGTCTC | ATGCACGGCA | TCTGGGAATC | CCCCTCCACA | GATCATGTGG  | 2100 |
| 15 | TTTAAAGATA | ATGAGACCCT | TGTAGAAGAC | TCAGGCATTG | TATTGAAGGA | TGGGAACCGG  | 2160 |
|    | AACCTCACTA | TCCGCAGAGT | GAGGAAGGAG | GACGAAGGCC | TCTACACCTG | CCAGGCATGC  | 2220 |
| 20 | AGTGTTCCTG | GCTGTGCAAA | AGTGGAGGCA | TTTTTCATAA | TAGAAGGTGC | CCAGGAAAAG  | 2280 |
|    | ACGAACTTGG | AAATCATTAT | TCTAGTAGGC | ACGGCGGTGA | TTGCCATGTT | CTTCTGGCTA  | 2340 |
|    | CTTCTTGTC  | TCATCCTACG | GACCGTTAAG | CGGGCCAATG | GAGGGGAACT | GAAGACAGGG  | 2400 |
| 25 | TACCTGTCCA | TCGTCATGGA | TCCAGATGAA | CTCCCATTGG | ATGAACATTG | TGAACGACTG  | 2460 |
|    | CCTTATGATG | CCAGCAAATG | GGAATTCCCC | AGAGACCGGC | TGAAGCTAGG | TAAGCCTCTT  | 2520 |
| 30 | GGCCGTGGTG | CCTTTGGCCA | AGTGATTGAA | GCAGATGCCT | TTGGAATTGA | CAAGACAGCA  | 2580 |
|    | ACTTGCAGGA | CAGTAGCAGT | CAAAATGTTG | AAAGAAGGAG | CAACACACAG | TGAGCATCGA  | 2640 |
|    | GCTCTCATGT | CTGAACTCAA | GATCCTCATT | CATATTGGTC | ACCATCTCAA | TGTGGTCAAC  | 2700 |
| 35 | CTTCTAGGTG | CCTGTACCAA | GCCAGGAGGG | CCACTCATGG | TGATTGTGGA | ATTCTGCAAA  | 2760 |
|    | TTTGGAACC  | TGTCCACTTA | CCTGAGGAGC | AAGAGAAATG | AATTTGTCCC | CTACAAGACC  | 2820 |
| 40 | AAAGGGGCAC | GATTCCGTCA | AGGGAAAGAC | TACGTTGGAG | CAATCCCTGT | GGATCTGAAA  | 2880 |
|    | CGGCGCTTGG | ACAGCATCAC | CAGTAGCCAG | AGCTCAGCCA | GCTCTGGATT | TGTGGAGGAG  | 2940 |
|    | AAGTCCCTCA | GTGATGTAGA | AGAAGAGGAA | GCTCCTGAAG | ATCTGTATAA | GGACTTCCTG  | 3000 |
| 45 | ACCTTGAGC  | ATCTCATCTG | TTACAGCTTC | CAAGTGGCTA | AGGGCATGGA | GTTCTTGGCA  | 3060 |
|    | TCGCGAAAGT | GTATCCACAG | GGACCTGGCG | GCACGAAATA | TCCTCTTATC | GGAGAAGAAC  | 3120 |
| 50 | GTGGTTAAAA | TCTGTGACTT | TGGCTTGGCC | CGGGATATTT | ATAAAGATCC | AGATTATGTC  | 3180 |
|    | AGAAAAGGAG | ATGCTCGCCT | CCCTTTGAAA | TGGATGGCCC | CAGAAACAAT | TTTTGACAGA  | 3240 |
|    | GTGTACACAA | TCCAGAGTGA | CGTCTGGTCT | TTTGGTGTTC | TGCTGTGGGA | AATATTTTCC  | 3300 |
| 55 | TTAGGTGCTT | CTCCATATCC | TGGGGTAAAG | ATTGATGAAG | AATTTTGTAG | GCGATTGAAA  | 3360 |
|    | GAAGGAACTA | GAATGAGGGC | CCCTGATTAT | ACTACACCAG | AAATGTACCA | GACCATGCTG  | 3420 |

GACTGCTGGC ACGGGGAGCC CAGTCAGAGA CCCACGTTTT CAGAGTTGGT GGAACATTTG 3480  
 GGAAATCTCT TGCAAGCTAA TGCTCAGCAG GATGGCAAAG ACTACATTGT TCTTCCGATA 3540  
 5 TCAGAGACTT TGAGCATGGA AGAGGATTCT GGACTCTCTC TGCCTACCTC ACCTGTTTCC 3600  
 TGTATGGAGG AGGAGGAAGT ATGTGACCCC AAATTCCATT ATGACAACAC AGCAGGAATC 3660  
 10 AGTCAGTATC TGCAGAACAG TAAGCGAAAG AGCCGGCCTG TGAGTGTAAG AACATTTGAA 3720  
 GATATCCCGT TAGAAGAACC AGAAGTAAAA GTAATCCCAG ATGACAACCA GACGGACAGT 3780  
 GGTATGGTTC TTGCCTCAGA AGAGCTGAAA ACTTTGGAAG ACAGAACCAA ATTATCTCCA 3840  
 15 TCTTTTGGTG GAATGGTGCC CAGCAAAAGC AGGGAGTCTG TGGCATCTGA AGGCTCAAAC 3900  
 CAGACAAGCG GCTACCAGTC CGGATATCAC TCCGATGACA CAGACACCAC CGTGTACTCC 3960  
 AGTGAGGAAG CAGAACTTTT AAAGCTGATA GAGATTGGAG TGCAAACCGG TAGCACAGCC 4020  
 20 CAGATTCTCC AGCCTGACTC GGGGACCACA CTGAGCTCTC CTCCTGTTTA A 4071

## (2) INFORMATION FOR SEQ ID NO:2:

25 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1356 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
 Met Glu Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu  
 1 5 10 15  
 35 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro  
 20 25 30  
 40 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr  
 35 40 45  
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro  
 50 55 60  
 45 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser  
 65 70 75 80  
 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn  
 50 85 90 95  
 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser  
 100 105 110  
 55 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser  
 115 120 125  
 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys  
 130 135 140

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|    | Thr | Val | Val | Ile | Pro | Cys | Leu | Gly | Ser | Ile | Ser | Asn | Leu | Asn | Val | Ser |  |
|    | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| 5  | Leu | Cys | Ala | Arg | Tyr | Pro | Glu | Lys | Arg | Phe | Val | Pro | Asp | Gly | Asn | Arg |  |
|    |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
|    | Ile | Ser | Trp | Asp | Ser | Lys | Lys | Gly | Phe | Thr | Ile | Pro | Ser | Tyr | Met | Ile |  |
| 10 |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
|    | Ser | Tyr | Ala | Gly | Met | Val | Phe | Cys | Glu | Ala | Lys | Ile | Asn | Asp | Glu | Ser |  |
|    |     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| 15 | Tyr | Gln | Ser | Ile | Met | Tyr | Ile | Val | Val | Val | Val | Gly | Tyr | Arg | Ile | Tyr |  |
|    | 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
|    | Asp | Val | Val | Leu | Ser | Pro | Ser | His | Gly | Ile | Glu | Leu | Ser | Val | Gly | Glu |  |
|    | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| 20 | Lys | Leu | Val | Leu | Asn | Cys | Thr | Ala | Arg | Thr | Glu | Leu | Asn | Val | Gly | Ile |  |
|    |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
|    | Asp | Phe | Asn | Trp | Glu | Tyr | Pro | Ser | Ser | Lys | His | Gln | His | Lys | Lys | Leu |  |
| 25 |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
|    | Val | Asn | Arg | Asp | Leu | Lys | Thr | Gln | Ser | Gly | Ser | Glu | Met | Lys | Lys | Phe |  |
|    |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| 30 | Leu | Ser | Thr | Leu | Thr | Ile | Asp | Gly | Val | Thr | Arg | Ser | Asp | Gln | Gly | Leu |  |
|    | 290 |     |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
|    | Tyr | Thr | Cys | Ala | Ala | Ser | Ser | Gly | Leu | Met | Thr | Lys | Lys | Asn | Ser | Thr |  |
|    | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| 35 | Phe | Val | Arg | Val | His | Glu | Lys | Pro | Phe | Val | Ala | Phe | Gly | Ser | Gly | Met |  |
|    |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
|    | Glu | Ser | Leu | Val | Glu | Ala | Thr | Val | Gly | Glu | Arg | Val | Arg | Ile | Pro | Ala |  |
| 40 |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
|    | Lys | Tyr | Leu | Gly | Tyr | Pro | Pro | Pro | Glu | Ile | Lys | Trp | Tyr | Lys | Asn | Gly |  |
|    |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| 45 | Ile | Pro | Leu | Glu | Ser | Asn | His | Thr | Ile | Lys | Ala | Gly | His | Val | Leu | Thr |  |
|    | 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |
|    | Ile | Met | Glu | Val | Ser | Glu | Arg | Asp | Thr | Gly | Asn | Tyr | Thr | Val | Ile | Leu |  |
|    | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |
| 50 | Thr | Asn | Pro | Ile | Ser | Lys | Glu | Lys | Gln | Ser | His | Val | Val | Ser | Leu | Val |  |
|    |     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |
|    | Val | Tyr | Val | Pro | Pro | Gln | Ile | Gly | Glu | Lys | Ser | Leu | Ile | Ser | Pro | Val |  |
| 55 |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |  |
|    | Asp | Ser | Tyr | Gln | Tyr | Gly | Thr | Thr | Gln | Thr | Leu | Thr | Cys | Thr | Val | Tyr |  |
|    |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |

|    |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|    | Ala | Ile | Pro | Pro | Pro | His | His | Ile | His | Trp | Tyr | Trp | Gln | Leu | Glu | Glu |  |
|    | 450 |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |
| 5  | Glu | Cys | Ala | Asn | Glu | Pro | Ser | Gln | Ala | Val | Ser | Val | Thr | Asn | Pro | Tyr |  |
|    | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |  |
|    | Pro | Cys | Glu | Glu | Trp | Arg | Ser | Val | Glu | Asp | Phe | Gln | Gly | Gly | Asn | Lys |  |
|    |     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |  |
| 10 | Ile | Glu | Val | Asn | Lys | Asn | Gln | Phe | Ala | Leu | Ile | Glu | Gly | Lys | Asn | Lys |  |
|    |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |  |
|    | Thr | Val | Ser | Thr | Leu | Val | Ile | Gln | Ala | Ala | Asn | Val | Ser | Ala | Leu | Tyr |  |
| 15 |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |  |
|    | Lys | Cys | Glu | Ala | Val | Asn | Lys | Val | Gly | Arg | Gly | Glu | Arg | Val | Ile | Ser |  |
|    |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |  |
| 20 | Phe | His | Val | Thr | Arg | Gly | Pro | Glu | Ile | Thr | Leu | Gln | Pro | Asp | Met | Gln |  |
|    | 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |  |
|    | Pro | Thr | Glu | Gln | Glu | Ser | Val | Ser | Leu | Trp | Cys | Thr | Ala | Asp | Arg | Ser |  |
|    |     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |  |
| 25 | Thr | Phe | Glu | Asn | Leu | Thr | Trp | Tyr | Lys | Leu | Gly | Pro | Gln | Pro | Leu | Pro |  |
|    |     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |  |
|    | Ile | His | Val | Gly | Glu | Leu | Pro | Thr | Pro | Val | Cys | Lys | Asn | Leu | Asp | Thr |  |
| 30 |     |     | 595 |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |  |
|    | Leu | Trp | Lys | Leu | Asn | Ala | Thr | Met | Phe | Ser | Asn | Ser | Thr | Asn | Asp | Ile |  |
|    |     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |  |
| 35 | Leu | Ile | Met | Glu | Leu | Lys | Asn | Ala | Ser | Leu | Gln | Asp | Gln | Gly | Asp | Tyr |  |
|    | 625 |     |     |     |     | 630 |     |     |     |     | 635 |     |     |     |     | 640 |  |
|    | Val | Cys | Leu | Ala | Gln | Asp | Arg | Lys | Thr | Lys | Lys | Arg | His | Cys | Val | Val |  |
|    |     |     |     |     | 645 |     |     |     |     | 650 |     |     |     |     | 655 |     |  |
| 40 | Arg | Gln | Leu | Thr | Val | Leu | Glu | Arg | Val | Ala | Pro | Thr | Ile | Thr | Gly | Asn |  |
|    |     |     |     | 660 |     |     |     |     | 665 |     |     |     |     | 670 |     |     |  |
|    | Leu | Glu | Asn | Gln | Thr | Thr | Ser | Ile | Gly | Glu | Ser | Ile | Glu | Val | Ser | Cys |  |
| 45 |     |     | 675 |     |     |     |     | 680 |     |     |     |     | 685 |     |     |     |  |
|    | Thr | Ala | Ser | Gly | Asn | Pro | Pro | Pro | Gln | Ile | Met | Trp | Phe | Lys | Asp | Asn |  |
|    |     | 690 |     |     |     | 695 |     |     |     |     |     | 700 |     |     |     |     |  |
| 50 | Glu | Thr | Leu | Val | Glu | Asp | Ser | Gly | Ile | Val | Leu | Lys | Asp | Gly | Asn | Arg |  |
|    | 705 |     |     |     |     | 710 |     |     |     |     | 715 |     |     |     |     | 720 |  |
|    | Asn | Leu | Thr | Ile | Arg | Arg | Val | Arg | Lys | Glu | Asp | Glu | Gly | Leu | Tyr | Thr |  |
|    |     |     |     | 725 |     |     |     |     |     | 730 |     |     |     |     | 735 |     |  |
| 55 | Cys | Gln | Ala | Cys | Ser | Val | Leu | Gly | Cys | Ala | Lys | Val | Glu | Ala | Phe | Phe |  |
|    |     |     |     | 740 |     |     |     |     | 745 |     |     |     |     | 750 |     |     |  |

|    |      |      |     |     |      |      |      |      |     |      |      |      |      |     |      |      |  |
|----|------|------|-----|-----|------|------|------|------|-----|------|------|------|------|-----|------|------|--|
|    | Ile  | Ile  | Glu | Gly | Ala  | Gln  | Glu  | Lys  | Thr | Asn  | Leu  | Glu  | Ile  | Ile | Ile  | Leu  |  |
|    |      |      | 755 |     |      |      |      | 760  |     |      |      |      | 765  |     |      |      |  |
| 5  | Val  | Gly  | Thr | Ala | Val  | Ile  | Ala  | Met  | Phe | Phe  | Trp  | Leu  | Leu  | Leu | Val  | Ile  |  |
|    |      | 770  |     |     |      |      | 775  |      |     |      |      | 780  |      |     |      |      |  |
|    | Ile  | Leu  | Arg | Thr | Val  | Lys  | Arg  | Ala  | Asn | Gly  | Gly  | Glu  | Leu  | Lys | Thr  | Gly  |  |
|    | 785  |      |     |     |      | 790  |      |      |     |      | 795  |      |      |     |      | 800  |  |
| 10 | Tyr  | Leu  | Ser | Ile | Val  | Met  | Asp  | Pro  | Asp | Glu  | Leu  | Pro  | Leu  | Asp | Glu  | His  |  |
|    |      |      |     |     | 805  |      |      |      |     | 810  |      |      |      |     | 815  |      |  |
|    | Cys  | Glu  | Arg | Leu | Pro  | Tyr  | Asp  | Ala  | Ser | Lys  | Trp  | Glu  | Phe  | Pro | Arg  | Asp  |  |
| 15 |      |      |     | 820 |      |      |      |      | 825 |      |      |      |      | 830 |      |      |  |
|    | Arg  | Leu  | Lys | Leu | Gly  | Lys  | Pro  | Leu  | Gly | Arg  | Gly  | Ala  | Phe  | Gly | Gln  | Val  |  |
|    |      |      | 835 |     |      |      |      | 840  |     |      |      |      | 845  |     |      |      |  |
| 20 | Ile  | Glu  | Ala | Asp | Ala  | Phe  | Gly  | Ile  | Asp | Lys  | Thr  | Ala  | Thr  | Cys | Arg  | Thr  |  |
|    | 850  |      |     |     |      |      | 855  |      |     |      |      | 860  |      |     |      |      |  |
|    | Val  | Ala  | Val | Lys | Met  | Leu  | Lys  | Glu  | Gly | Ala  | Thr  | His  | Ser  | Glu | His  | Arg  |  |
|    | 865  |      |     |     |      | 870  |      |      |     |      | 875  |      |      |     |      | 880  |  |
| 25 | Ala  | Leu  | Met | Ser | Glu  | Leu  | Lys  | Ile  | Leu | Ile  | His  | Ile  | Gly  | His | His  | Leu  |  |
|    |      |      |     |     | 885  |      |      |      |     | 890  |      |      |      |     | 895  |      |  |
|    | Asn  | Val  | Val | Asn | Leu  | Leu  | Gly  | Ala  | Cys | Thr  | Lys  | Pro  | Gly  | Gly | Pro  | Leu  |  |
| 30 |      |      |     | 900 |      |      |      |      | 905 |      |      |      |      | 910 |      |      |  |
|    | Met  | Val  | Ile | Val | Glu  | Phe  | Cys  | Lys  | Phe | Gly  | Asn  | Leu  | Ser  | Thr | Tyr  | Leu  |  |
|    |      |      | 915 |     |      |      |      | 920  |     |      |      |      | 925  |     |      |      |  |
| 35 | Arg  | Ser  | Lys | Arg | Asn  | Glu  | Phe  | Val  | Pro | Tyr  | Lys  | Thr  | Lys  | Gly | Ala  | Arg  |  |
|    |      | 930  |     |     |      |      | 935  |      |     |      |      | 940  |      |     |      |      |  |
|    | Phe  | Arg  | Gln | Gly | Lys  | Asp  | Tyr  | Val  | Gly | Ala  | Ile  | Pro  | Val  | Asp | Leu  | Lys  |  |
|    | 945  |      |     |     |      | 950  |      |      |     |      | 955  |      |      |     |      | 960  |  |
| 40 | Arg  | Arg  | Leu | Asp | Ser  | Ile  | Thr  | Ser  | Ser | Gln  | Ser  | Ser  | Ala  | Ser | Ser  | Gly  |  |
|    |      |      |     |     | 965  |      |      |      |     | 970  |      |      |      |     | 975  |      |  |
|    | Phe  | Val  | Glu | Glu | Lys  | Ser  | Leu  | Ser  | Asp | Val  | Glu  | Glu  | Glu  | Glu | Ala  | Pro  |  |
| 45 |      |      |     | 980 |      |      |      |      | 985 |      |      |      |      | 990 |      |      |  |
|    | Glu  | Asp  | Leu | Tyr | Lys  | Asp  | Phe  | Leu  | Thr | Leu  | Glu  | His  | Leu  | Ile | Cys  | Tyr  |  |
|    |      |      | 995 |     |      |      |      | 1000 |     |      |      |      | 1005 |     |      |      |  |
| 50 | Ser  | Phe  | Gln | Val | Ala  | Lys  | Gly  | Met  | Glu | Phe  | Leu  | Ala  | Ser  | Arg | Lys  | Cys  |  |
|    |      | 1010 |     |     |      |      | 1015 |      |     |      |      | 1020 |      |     |      |      |  |
|    | Ile  | His  | Arg | Asp | Leu  | Ala  | Ala  | Arg  | Asn | Ile  | Leu  | Leu  | Ser  | Glu | Lys  | Asn  |  |
|    | 1025 |      |     |     |      | 1030 |      |      |     |      | 1035 |      |      |     |      | 1040 |  |
| 55 | Val  | Val  | Lys | Ile | Cys  | Asp  | Phe  | Gly  | Leu | Ala  | Arg  | Asp  | Ile  | Tyr | Lys  | Asp  |  |
|    |      |      |     |     | 1045 |      |      |      |     | 1050 |      |      |      |     | 1055 |      |  |

|    |   |                |
|----|---|----------------|
|    | Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys Trp Met |                |
|    | 1060  | 1065 1070      |
| 5  | Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln Ser Asp Val |                |
|    | 1075  | 1080 1085      |
|    | Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser |                |
|    | 1090  | 1095 1100      |
| 10 | Pro Tyr Pro Gly Val Lys Ile Asp Glu Glu Phe Cys Arg Arg Leu Lys |                |
|    | 1105  | 1110 1115 1120 |
|    | Glu Gly Thr Arg Met Arg Ala Pro Asp Tyr Thr Thr Pro Glu Met Tyr |                |
| 15 |   | 1125 1130 1135 |
|    | Gln Thr Met Leu Asp Cys Trp His Gly Glu Pro Ser Gln Arg Pro Thr |                |
|    | 1140  | 1145 1150      |
| 20 | Phe Ser Glu Leu Val Glu His Leu Gly Asn Leu Leu Gln Ala Asn Ala |                |
|    | 1155  | 1160 1165      |
|    | Gln Gln Asp Gly Lys Asp Tyr Ile Val Leu Pro Ile Ser Glu Thr Leu |                |
|    | 1170  | 1175 1180      |
| 25 | Ser Met Glu Glu Asp Ser Gly Leu Ser Leu Pro Thr Ser Pro Val Ser |                |
|    | 1185  | 1190 1195 1200 |
|    | Cys Met Glu Glu Glu Glu Val Cys Asp Pro Lys Phe His Tyr Asp Asn |                |
| 30 |   | 1205 1210 1215 |
|    | Thr Ala Gly Ile Ser Gln Tyr Leu Gln Asn Ser Lys Arg Lys Ser Arg |                |
|    | 1220  | 1225 1230      |
| 35 | Pro Val Ser Val Lys Thr Phe Glu Asp Ile Pro Leu Glu Glu Pro Glu |                |
|    | 1235  | 1240 1245      |
|    | Val Lys Val Ile Pro Asp Asp Asn Gln Thr Asp Ser Gly Met Val Leu |                |
|    | 1250  | 1255 1260      |
| 40 | Ala Ser Glu Glu Leu Lys Thr Leu Glu Asp Arg Thr Lys Leu Ser Pro |                |
|    | 1265  | 1270 1275 1280 |
|    | Ser Phe Gly Gly Met Val Pro Ser Lys Ser Arg Glu Ser Val Ala Ser |                |
| 45 |   | 1285 1290 1295 |
|    | Glu Gly Ser Asn Gln Thr Ser Gly Tyr Gln Ser Gly Tyr His Ser Asp |                |
|    | 1300  | 1305 1310      |
| 50 | Asp Thr Asp Thr Thr Val Tyr Ser Ser Glu Glu Ala Glu Leu Leu Lys |                |
|    | 1315  | 1320 1325      |
|    | Leu Ile Glu Ile Gly Val Gln Thr Gly Ser Thr Ala Gln Ile Leu Gln |                |
|    | 1330  | 1335 1340      |
| 55 | Pro Asp Ser Gly Thr Thr Leu Ser Ser Pro Pro Val                 |                |
|    | 1345  | 1350 1355      |



(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

10 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

15 GGAATTCCAT CCAAGCGCA AATGTGTC 28

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 GGAATTCGA GTCTTCTACA AGGGTCTC 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

40 (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

45 TTATGACAAC ACAGCAGG 18

(2) INFORMATION FOR SEQ ID NO:6:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 TTGGATCCTC GAGTTGGGGT GTGGATGC 28

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 GGATCCAGAT GAACTCCCAT TG 22

(2) INFORMATION FOR SEQ ID NO:8:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

35 GTCGACTTAG TCTTTGCCAT CCTGCTGAGC 30

40

## WHAT IS CLAIMED:

1. A purified nucleic acid molecule encoding a human KDR protein which consists essentially of the nucleotide sequence

5 ATGGAGAGCAAGGTGCTGCTGGCCGTCGCCCTGTGGCTCTGCGTGGAGACCCGGGCCGCCTCTGTGGGT  
TTGCCCTAGTGTTCCTCTTGATCTGCCCAGGCTCAGCATACAAAAAGACATACTTACAATTAAGGCTAAT  
ACAACCTCTTCAAATTACTTGCAGGGGACAGAGGGACTTGGACTGGCTTTGGCCCAATAATCAGAGTGGC  
AGTGAGCAAAGGGTGGAGGTGACTGAGTGCAGCGATGGCCTCTTCTGTAAGACACTCACAATTCAAAA  
GTGATCGGAAATGACACTGGAGCCTACAAGTGCTTCTACCGGGAAACTGACTTGGCCTCGGTCATTTAT  
10 GTCTATGTTCAAGATTACAGATCTCCATTTATTGCTTCTGTAGTGACCAACATGGAGTCGTGTACATT  
ACTGAGAACAAAAACAAAACCTGTGGTGATTCCATGTCTCGGGTCCATTTCAAATCTCAACGTGTCACTT  
TGTGCAAGATACCCAGAAAAGAGATTTGTTCTGATGGTAACAGAATTTCTTGGGACAGCAAGAAGGGC  
TTTACTATTCCCAGCTACATGATCAGCTATGCTGGCATGGTCTTCTGTGAAGCAAAAATTAATGATGAA  
AGTTACCAGTCTATTATGTACATAGTTGTCGTTGTAGGGTATAGGATTTATGATGTGGTTCTGAGTCCG  
15 TCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAAT  
GTGGGGATTGACTTCAACTGGGAATACCCCTTCTTGAAGCATCAGCATAAGAACTTGTAAACCGAGAC  
CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAAACCCGG  
AGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTC  
AGGGTCCATGAAAAACCTTTTGTGCTTTTGAAGTGGCATGGAATCTCTGGTGGAAAGCCACGGTGGGG  
20 GAGCGTGTGAGAAATCCCTGCGAAGTACCTTGGTTACCCACCCCCAGAAATAAAATGGTATAAAAATGGA  
ATACCCCTTGAGTCCAATCACACAATTAAAGCGGGGCATGTAAGTACGATTATGGAAGTGAAGTGAAGA  
GACACAGGAAATTACACTGTCATCCTTACCAATCCCATTTCAAAGGAGAAGCAGAGCCATGTGGTCTCT  
CTGGTTGTGTATGTCCACCCCAGATTGGTGAGAAATCTCTAATCTCTCCTGTGGATTCTTACCAGTAC  
GGCACCCTCAAACGCTGACATGTACGGTCTATGCCATTCTTCCCCGCATCACATCCACTGGTATTGG  
25 CAGTTGGAGGAAGAGTGCGCCAACGAGCCCAGCCAAGCTGTCTCAGTGACAAACCCATACCTTGTGAA  
GAATGGAGAAAGTGTGGAGGACTTCCAGGGAGGAAATAAAATTTGAAGTTAATAAAAAATCAATTTGCTCTA  
ATTGAAGGAAAAAACAAAACCTGTAAGTACCCTTGTATCCAAGCGGCAAAATGTGTCAGCTTTGTACAAA  
TGTGAAGCGGTCAACAAAGTCGGGAGAGGAGAGAGGGTGTATCTCCTTCCACGTGACCAGGGGTCTGAA  
ATTACTTTGCAACCTGACATGCAGCCCACTGAGCAGGAGAGCGTGTCTTTGTGGTGCCTGCAGACAGA  
30 TCTACGTTTGGAGAACCTCACATGGTACAAGCTTGGCCACAGCCTCTGCCAATCCATGTGGGAGAGTTG  
CCCACACCTGTTTGCAGAAGCTTGGATACTCTTTGGAAATTGAATGCCACCATGTTCTCTAATAGCACA  
AATGACATTTTGATCATGGAGCTTAAGAATGCATCCTTGCAGGACCAAGGAGACTATGTCTGCCTTGCT  
CAAGACAGGAAGACCAAGAAAAGACATTGCGTGGTCAGGCAGCTCACAGTCTAGAGCGTGTGGCACCC  
ACGATCACAGGAAACCTGGAGAATCAGACGACAAGTATTGGGGAAAGCATCGAAGTCTCATGCACGGCA  
35 TCTGGGAATCCCCCTCCACAGATCATGTGGTTTAAAGATAATGAGACCCTTGTAAGAAGACTCAGGCATT  
GTATTGAAGGATGGGAACCGGAACCTCACTATCCGCAGAGTGAGGAAGGAGGACGAAGGCCTCTACACC

TGCCAGGCATGCAGTGTCTTGGCTGTGCAAAAGTGGAGGCATTTTTCATAATAGAAGGTGCCCAGGAA  
 AAGACGAACTTGGAAATCATTATTCTAGTAGGCACGGCGGTGATTGCCATGTTCTTCTGGCTACTTCTT  
 GTCATCATCTTACGGACCGTTAAGCGGGCCAATGGAGGGGAAGTGAAGACAGGCTACTTGTCCATCGTC  
 ATGGATCCAGATGAACTCCCATTGGATGAACATTGTGAACGACTGCCTTATGATGCCAGCAAAATGGGAA  
 5 TTCCCCAGAGACCGGCTGAAGCTAGGTAAGCCTCTTGGCCGTGGTGCCTTTGGCCAAGTGATTGAAGCA  
 GATGCCTTTTGAATTGACAAGACAGCAACTTGCAGGACAGTAGCAGTCAAAATGTTGAAAGAAGGAGCA  
 ACACACAGTGAGCATCGAGCTCTCATGTCTGAACTCAAGATCCTCATTTCATATTGGTCACCATCTCAAT  
 GTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAGGAGGGCCACTCATGGTGATTGTGGAATTTCTGCAAA  
 TTTGGAAACCTGTCCACTTACCTGAGGAGCAAGAGAAATGAATTTGTCCCTACAAGACCAAGGGGCA  
 10 CGATTCCGTCAAGGGAAAGACTACGTTGGAGCAATCCCTGTGGATCTGAAACGGCGCTTGGACAGCATC  
 ACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTTGTGGAGGAGAAGTCCCTCAGTGATGTAGAAGAAGAG  
 GAAGCTCCTGAAGATCTGTATAAGGACTTCCTGACCTTGGAGCATCTCATCTGTTACAGCTTCCAAGTG  
 GCTAAGGGCATGGAGTTCTTGGCATCGCGAAAGTGTATCCACAGGGACCTGGCGGCACGAAATATCCTC  
 TTATCGGAGAAGAACGTGGTTAAAAATCTGTGACTTTGGCTTGGCCCGGGATATTTATAAAGATCCAGAT  
 15 TATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGATGGCCCCAGAAACAATTTTGGACAGAGTG  
 TACACAATCCAGAGTGACGTCTGGTCTTTTGGTGTGTTTGTGCTGTGGGAAATATTTTCTTAGGTGCTTCT  
 CCATATCCTGGGGTAAAGATTGATGAAGAATTTTGTAGGCGATTGAAAGAAGGAAGTGAATGAGGGCC  
 CCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGGCACGGGGAGCCAGTCAGAGA  
 CCCACGTTTTTCAGAGTTGGTGAACATTTGGGAAATCTCTTGCAAGCTAATGCTCAGCAGGATGGCAAA  
 20 GACTACATTGTTCTTCCGATATCAGAGACTTTGAGCATGGAAGAGGATTCTGGACTCTCTCTGCCTACC  
 TCACCTGTTTCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCATTATGACAACACAGCAGGA  
 ATCAGTCAGTATCTGCAGAACAGTAAGCGAAAGAGCCGGCCTGTGAGTGTAACAAATTTGAAGATATC  
 CCGTTAGAAGAACCAGAAGTAAAGTAATCCCAGATGACAACCAGACGAGTGGTATGGTTCTTGCC  
 TCAGAAGAGCTGAAAACCTTTGGAAGACAGAACCAAATTATCTCCATCTTTTGGTGAATGGTGCCAGC  
 25 AAAAGCAGGGAGTCTGTGGCATCTGAAGGCTCAAACCAGACAAGCGGCTACCAGTCCGGATATCACTCC  
 GATGACACAGACACCACCGTGTACTCCAGTGAGGAAGCAGAAGTAAAGCTGATAGAGATTGGAGTG  
 CAAACCGGTAGCACAGCCAGATTCTCCAGCCTGACTCGGGGACCACACTGAGCTCTCCTCCTGTTTAA  
 (SEQ ID NO:1), wherein said nucleic acid molecule encodes a human  
 KDR protein or biologically active form thereof where at least amino acid  
 30 residues selected from the group consisting of Val at position 848, Glu at  
 position 498, Ala at position 772, Arg at position 787, Lys at position 835  
 and Ser at position 1347 are present in said protein.

2. A purified DNA molecule encoding human KDR  
 35 wherein said DNA molecule encodes a protein consisting essentially of  
 the amino acid sequence:

MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQRDLDWLWPNQSG  
 SEQRVEVTECDGLFCKTLTIPKVIGNDTGAYKCFYRETDLASVIYVYVQDYRSPFIASVSDQHGVVYI  
 TENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCEAKINDE  
 SYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD  
 5 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVG  
 ERVRIPAKYLGYPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSEEDTGNYTVILTNPISKEKQSHVVS  
 LVVYVPPQIGESLISPVDYQYGTQTTLCTVYAIPPHHHIHWYQLEEECANEPSQAVSVTNPYPC  
 EWRSEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPE  
 ITLQPDMPTEQESVSLWCTADRSTFENLTWYKLGPPPIHVGEPLTPVCKNLDLWKLNATMFSNST  
 10 NDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVRQLTVLERVAPTITGNLENQTTSIGESIEVSCTA  
 SGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIIRVRKEDEGLYTCQACSVLGCACVEAFFIIEGAQE  
 KTNLEIIILVGTAVIAMFFWLLLVIIILRTVVRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWE  
 FPRDLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHGHHLN  
 VVNLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKTKGARFRQGDYVGAIPVDLKRRLDSI  
 15 TSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRCKIHRDLAARNIL  
 LSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGAS  
 PYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGK  
 DYIVLPISETLSMEEDSGLSLPTSPVSCMEEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDI  
 PLEEPEVKVIPDDNQTDGMLVASEELKTLEDRTKLSPSFGGMVPSKSRESVASEGSNQTSQYQSGYHS  
 20 DDTDTTVYSSEEAELLKLEIGVQTGSTAQILQPDSTLSSPPV, as set forth in a three-  
 letter abbreviation in SEQ ID NO:2 and containing amino acid residues  
 selected from the group consisting of Val at position 848, Glu at position  
 498, Ala at position 772, Arg at position 787, Lys at position 835 and Ser at  
 position 1347.

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3. An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 1.

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4. An expression vector of claim 3 which is a eukaryotic expression vector.

5. An expression vector of claim 3 which is a prokaryotic expression vector.

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6. A host cell which expresses a recombinant human KDR protein wherein said host cell contains the expression vector of claim 3.

5 7. A host cell which expresses a recombinant human KDR protein wherein said host cell contains the expression vector of claim 4.

10 8. A host cell which expresses a recombinant human KDR protein wherein said host cell contains the expression vector of claim 5.

15 9. A host cell of claim 6 wherein said human KDR protein is overexpressed from said expression vector.

10. A host cell of claim 7 wherein said human KDR protein is overexpressed from said expression vector.

20 11. A host cell of claim 8 wherein said human KDR protein is overexpressed from said expression vector.

12. A subcellular membrane fraction obtained from the host cell of claim 9 which contains recombinant human KDR protein.

25 13. A subcellular membrane fraction obtained from the host cell of claim 10 which contains recombinant human KDR protein.

30 14. A subcellular membrane fraction obtained from the host cell of claim 11 which contains recombinant human KDR protein.

15. A purified DNA molecule which consists of the nucleotide sequence:

ATGGAGAGCAAGGTGCTGCTGGCCGTCGCCCTGTGGCTCTGCGTGGAGACCCGGGCCGCTCTGTGGGTT  
TGCCTAGTGTCTTCTCTTGATCTGCCCAGGCTCAGCATACAAAAAGACATACTTACAATTAAGGCTAATAC  
35 AACTCTTCAAATTACTTGCAGGGGACAGAGGGACTTGGACTGGCTTTGGCCCAATAATCAGAGTGGCAGT  
GAGCAAAGGGTGGAGGTGACTGAGTGCAGCGATGGCCTCTTCTGTAAGACACTCACAATTCCAAAAGTGA

TCGGAAATGACACTGGAGCCTACAAGTGCTTCTACCGGGAACTGACTTGGCCTCGGTCAATTTATGTCTA  
TGTTCAGATTACAGATCTCCATTTATTGCTTCTGTTAGTGACCAACATGGAGTCGTGTACATTACTGAG  
AACAAAAACAAAACGTGGTGATTCCATGTCTCGGGTCCATTTCAAATCTCAACGTGTCACTTTGTGCAA  
GATACCCAGAAAAGAGATTTGTTCCCTGATGGTAACAGAATTTCTGGGACAGCAAGAAGGGCTTTACTAT  
5 TCCCAGCTACATGATCAGCTATGCTGGCATGGTCTTCTGTGAAGCAAAAATTAATGATGAAAGTTACCAG  
TCTATTATGTACATAGTTGTCTGTTGTAGGGTATAGGATTTATGATGTGGTTCCTGAGTCCGTCTCATGGAA  
TTGAACTATCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACATAATGTGGGGATTGA  
CTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAACTTGTAAACCGAGACCTAAAAACCCAG  
TCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAAACCCGGAGTGACCAAGGAT  
10 TGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTCAGGGTCCATGAAAA  
ACCTTTTGTGCTTTTGGAGTGGCATGGAATCTCTGGTGGAAGCCACGGTGGGGGAGCGTGTGAGAATC  
CCTGCGAAGTACCTTGGTTACCCACCCCCAGAAATAAAATGGTATAAAAATGGAATACCCCTTGAGTCCA  
ATCACACAATTAAAGCGGGGCATGTACTGACGATTATGGAAGTGAGTGAAAGAGACACAGGAAATTACAC  
TGTCATCCTTACCAATCCCATTTCAAAGGAGAAGCAGAGCCATGTGGTCTCTCTGGTTGTGTATGTCCCA  
15 CCCCAGATTGGTGAGAAATCTCTAATCTCTCCTGTGGATTCTTACCAGTACGGCACCACTCAAACGCTGA  
CATGTACGGTCTATGCCATTCTCTCCCCGCATCACATCCACTGGTATTGGCAGTTGGAGGAAGAGTGC GC  
CAACGAGCCCAGCCAAGCTGTCTCAGTGACAAACCCATACCCCTTGTGAAGAATGGAGAAGTGTGGAGGAC  
TTCCAGGGAGGAAATAAAATTGAAGTTAATAAAAAATCAATTTGCTCTAATTGAAGGAAAAAACAAACTG  
TAAGTACCCCTTGTATCCAAGCGGCAAATGTGTGAGCTTTGTACAAATGTGAAGCGGTCAACAAAGTCGG  
20 GAGAGGAGAGAGGGTGATCTCCTTCCACGTGACCAGGGTCTTGAAATTACTTTGCAACCTGACATGCAG  
CCCACTGAGCAGGAGAGCGTGTCTTTGTGGTGCCTGCAGACAGATCTACGTTTGAGAACCTCACATGGT  
ACAAGCTTGGCCACAGCCTCTGCCAATCCATGTGGGAGAGTTGCCACACCTGTTTGCAAGAACTTGGA  
TACTCTTTGGAATTTGAATGCCACCATGTTCTCTAATAGCACAAATGACATTTTGTATCATGGAGCTTAAG  
AATGCATCCTTGCAGGACCAAGGAGACTATGTCTGCCTTGCTCAAGACAGGAAGACCAAGAAAAGACATT  
25 GCGTGGTCAGGCAGCTCACAGTCTAGAGCGTGTGGCACCCACGATCACAGGAAACCTGGAGAATCAGAC  
GACAAGTATTGGGGAAAGCATCGAAGTCTCATGCACGGCATCTGGGAATCCCCCTCCACAGATCATGTGG  
TTTAAAGATAATGAGACCCTTGTAGAAGACTCAGGCATTGTATTGAAGGATGGGAACCGGAACCTCACTA  
TCCGCAGAGTGAGGAAGGAGGACGAAGGCCTCTACACCTGCCAGGCATGCAGTGTCTTGGCTGTGCAAA  
AGTGGAGGCATTTTTTCATAATAGAAGGTGCCCAGGAAAAGACGAACCTTGGAATCATTATTCTAGTAGGC  
30 ACGGCGGTGATTGCCATGTTCTTCTGGCTACTTCTTGTCATCATCCTACGGACCGTTAAGCGGGCCAATG  
GAGGGGAACCTGAAGACAGGCTACTTGTCCATCGTCATGGATCCAGATGAACTCCCATTGGATGAACATTG  
TGAACGACTGCCTTATGATGCCAGCAAATGGGAATTCCCCAGAGACCGGCTGAAGCTAGGTAAGCCTCTT  
GGCCGTGGTGCCTTTGGCCAAGTGATTGAAGCAGATGCCTTTGGAATTGACAAGACAGCAACTTGCAGGA  
CAGTAGCAGTCAAATGTTGAAAGAAGGAGCAACACACAGTGAGCATCGAGCTCTCATGTCTGAACTCAA  
35 GATCCTCATTCATATTGGTCACCATCTCAATGTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAGGAGGG  
CCACTCATGGTGATTGTGGAATTCTGCAAATTTGGAAACCTGTCCACTTACCTGAGGAGCAAGAGAAATG

AATTTGTCCCCTACAAGACCAAAGGGGCACGATTCCCGTCAAGGGAAAGACTACGTTGGAGCAATCCCTGT  
 GGATCTGAAACGGCGCTTGGACAGCATCACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTTGTGGAGGAG  
 AAGTCCCTCAGTGATGTAGAAGAAGAGGAAGCTCCTGAAGATCTGTATAAGGACTTCCTGACCTTGGAGC  
 ATCTCATCTGTTACAGCTTCCAAGTGGCTAAGGGCATGGAGTTCTTGGCATCGCGAAAGTGATCCACAG  
 5 GGACCTGGCGGCACGAAATATCCTCTTATCGGAGAAGAACGTGGTTAAAATCTGTGACTTTGGCTTGGCC  
 CGGGATATTTATAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGATGGCCC  
 CAGAAACAATTTTTGACAGAGTGACACAATCCAGAGTGACGTCTGGTCTTTTGGTGTTTTGCTGTGGGA  
 AATATTTTCCTTAGGTGCTTCTCCATATCCTGGGGTAAAGATTGATGAAGAATTTTGTAGGCGATTGAAA  
 GAAGGAAC TAGAATGAGGGCCCCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGGC  
 10 ACGGGGAGCCCAGTCAGAGACCCACGTTTTTCAGAGTTGGTGGAACATTTGGGAAATCTCTTGCAAGCTAA  
 TGCTCAGCAGGATGGCAAAGACTACATTGTTCTTCCGATATCAGAGACTTTGAGCATGGAAGAGGATTCT  
 GGACTCTCTCTGCCTACCTCACCTGTTTCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCATT  
 ATGACAACACAGCAGGAATCAGTCAGTATCTGCAGAACAGTAAGCGAAAGAGCCGGCCTGTGAGTGATAA  
 AACATTTGAAGATATCCCGTTAGAAGAACCAGAAGTAAAAGTAATCCCAGATGACAACCAGACGGACAGT  
 15 GGTATGGTTCTTGCCTCAGAAGAGCTGAAAAC TTTGGAAGACAGAACC AAATTATCTCCATCTTTTGGTG  
 GAATGGTGCCAGCAAAGCAGGGAGTCTGTGGCATCTGAAGGCTCAAACCAGACAAGCGGCTACCAGTC  
 CGGATATCACTCCGATGACACAGACACCACCGTGTACTCCAGTGAGGAAGCAGAACTTTTAAAGCTGATA  
 GAGATTGGAGTGCAAACCGGTAGCACAGCCCAGATTCTCCAGCCTGACTCGGGGACCACACTGAGCTCTC  
 CTCCTGTTTAA, disclosed as SEQ ID NO:1.

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16. A purified human KDR protein which consists of the amino acid sequence

MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILT IKANTTLQITCRGQRDLWLWPNNQSG  
 SEQRVEVTECS DGLFCKTLTI PKVIGNDTGAYKCFYRETDLASVIYVYVQDYRSPFIASVSDQHGVVYI  
 25 TENKNKTVVIPCLGSISNLNVSLCARYPEKRFVPDGNRISWDSKKGFTIPSYMISYAGMVFCEAKINDE  
 SYQSIMYIVVVVGYRIYDVVLSPSHGIELSVGEKLVNCTARTELVNVDNFNWEYPSSKHQHKLVNRD  
 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGMESLVEATVG  
 ERVRIPAKYLGYPPPEIKWKNGIPLSNHTIKAGHVLTIMEVSEKDTGNYTVILTNPISKEKQSHVVS  
 LVVYVPPQIGEKSLIPVDSYQYGTQTTLCTVYAI PPPHHIHWWQLEEECANEPSQAVSVTNYPYCE  
 30 EWRSVEDFQGGNKIEVNKNQFALIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPE  
 ITLQPDMPTEQESVSLWCTADRSTFENLTWYKLGQPLPIHVGE LPTPVCKNLDTLWKL NATMFSNST  
 NDILIMELKNASLQDQGDYVCLAQDRKTKKRHCVVRLTVLERVAPTITGNLENQTTSIGESIEVSCTA  
 SGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTI RVRKEDEGLYTCQACSVLGCAKVEAFFIIEGAQE  
 KTNLEIIILVGTAVIAMFFWLLLVII LR TVKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWE  
 35 FPRDRCLKGLPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRAIMSELKILIHGHLN  
 VVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVYPYTKGARFRQGDYVGAIPVDLKRRLDSI



TSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFTLEHLICYSFQVAKGMEFLASRKC IHRDLAARNIL  
 LSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGAS  
 PYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANAQQDGK  
 DYIVLPISETLSMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVSVKTFEDI  
 5 PLEEPEVKVIPDDNQTDSGMVLASEELKTLEDRTKLSPSFGCMVPSKSRESVASEGSNQTSQYQSGYHS  
 DDTDTTVYSSEEAELLKLIEIGVQTGSTAQILQPDSTTLSSPPV, as set forth in three

letter abbreviation in SEQ ID NO:2 and containing amino acid residues  
 selected from the group consisting of Val at position 848, Glu at position  
 498, Ala at position 772, Arg at position 787, Lys at position 835 and Ser at  
 10 position 1347.

17. The purified human KDR protein of claim 16 as set  
 forth in SEQ ID NO:2.

15 18. A process for the expression of a human KDR protein  
 in a recombinant host cell, comprising:

(a) transfecting the expression vector of claim 3 into  
 a suitable host cell; and,

20

(b) culturing the host cells of step (a) under  
 conditions which allow expression of the human KDR protein from the  
 expression vector.

25 19. An expression vector for the expression of a human  
 KDR protein in a recombinant host cell wherein said expression vector  
 comprises the DNA molecule of claim 15.

30 20. A purified nucleic acid molecule encoding an  
 intracellular portion of a human KDR protein which comprises from  
 about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO:  
 2, wherein position 848 is a valine residue.

35 21. A purified nucleic acid molecule of claim 20 encoding  
 an intracellular portion of a human KDR protein which comprises from  
 about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO:

2, wherein position 772 is an alanine residue, position 787 is an arginine residue, position 835 is a lysine residue, position 848 is a valine residue and position 1347 is a serine residue.

5                   22.    An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 20.

10                   23.    An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 21.

15                   24.    A purified protein fragment which is an intracellular portion of a human KDR protein, comprising from about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO: 2, wherein position 848 is a valine residue.

20                   25.    A purified protein fragment of claim 24 which comprises from about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO: 2, wherein position 772 is an alanine residue, position 787 is an arginine residue, position 835 is a lysine residue, position 848 is a valine residue and position 1347 is a serine residue.

25                   26.    A purified nucleic acid molecule encoding an soluble KDR fusion protein which comprises from about amino acid 790 to about amino acid 1356 of human KDR as set forth in SEQ ID NO: 2, wherein position 848 is a valine residue.

30                   27.    A purified nucleic acid molecule of claim 26 wherein said KDR fusion protein comprises from about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO: 2, position 772 being an alanine residue, position 787 being an arginine residue, position 835 being a lysine residue, position 848 being a valine residue and position 1347 being a serine residue.

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28. A purified nucleic acid molecule of claim 27 which encodes GST-KDR.

5 29. An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 26.

10 30. An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 27.

15 31. An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 28.

20 32. A purified KDR fusion protein which is characterized by an intracellular portion of a human KDR protein, comprising from about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO: 2, wherein position 848 is a valine residue.

25 33. A purified KDR fusion protein of claim 32 which comprises from about amino acid 790 to about amino acid 1356 as set forth in SEQ ID NO: 2, wherein position 772 is an alanine residue, position 787 is an arginine residue, position 835 is a lysine residue, position 848 is a valine residue and position 1347 is a serine residue.

34. The purified KDR fusion protein of claim 33 which is GST-KDR.

30 35. A purified nucleic acid molecule encoding an extracellular portion of a human KDR protein which comprises from about amino acid 1 to about amino acid 644 as set forth in SEQ ID NO:2, wherein position 498 is a glutamic acid residue.

36. An expression vector for the expression of a human KDR protein in a recombinant host cell wherein said expression vector comprises the DNA molecule of claim 36.

5 37. A purified protein fragment which is an extracellular portion of a human KDR protein, comprising from about amino acid 1 to about amino acid 790 as set forth in SEQ ID NO: 2, wherein position 498 is a glutamic acid residue, position 772 is an alanine residue and position 787 is an arginine residue.

10 38. An isolated nucleic acid molecule of claim 20 wherein a termination codon is inserted such that the KDR open reading frame terminates at about Tyr 1175.

15 39. An isolated nucleic acid of claim 38 which is contained within a DNA vector, pBlueBacHis2B.

40. The DNA vector of claim 39 which is pBBH-KDR-1.

20 41. A method of selecting a compound which antagonizes human KDR which comprises a biological assay wherein a test compound is added in combination with a KDR protein or protein fragment and a substrate, said substrate being involved in a measurable interaction at a domain of interest within wild-type KDR such that a  
25 compound antagonist interacts with said KDR protein, resulting in a measurable decrease in KDR:substrate activity.

30 42. A method of claim 41 wherein said KDR protein is GST/KDR-1.

43. A method of claim 42 wherein said substrate is pEY.

35 44. A method of selecting a compound which is an agonist of human KDR which comprises a biological assay wherein a test compound is added in combination with a KDR protein or protein fragment and a substrate, said substrate being involved in a measurable

interaction at a domain of interest within wild-type KDR such that a compound antagonist interacts with said KDR protein, resulting in a measurable increase in KDR:substrate activity.

5                    45.    A method of claim 44 wherein said KDR protein is GST/KDR-1.

                  46.    A method of claim 45 wherein said substrate is pEY.

10

ATGGAGAGCAAGGTGCTGCTGGCCGTCGCCCTGTGGCTCTGCGTGGAGACCC  
GGGCCGCCTCTGTGGGTTTGCCTAGTGTTTCTTCTTGATCTGCCCAGGCTCAGCA  
TACAAAAAGACATACTTACAATTAAGGCTAATACTCTTCAAATTACTTGCAG  
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CAAAGGGTGGAGGTGACTGAGTGCAGCGATGGCCTCTTCTGTAAGACACTCAC  
AATTCACAAAAGTGATCGGAAATGACACTGGAGCCTACAAGTGCTTCTACCGGG  
AAACTGACTTGGCCTCGGTCAATTTATGTCTATGTTCAAGATTACAGATCTCCATT  
TATTGCTTCTGTAGTGACCAACATGGAGTCGTGTACATTACTGAGAACAAAAA  
CAAACTGTGGTGATTCCATGTCTCGGGTCCATTTCAAATCTCAACGTGTCACTT  
TGTGCAAGATACCCAGAAAAAGAGATTTGTTCTGATGGTAACAGAATTCCTGG  
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TTGTCGTTGTAGGGTATAGGATTTATGATGTGGTTCTGAGTCCGTCTCATGGAA  
TTGAACTATCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAAGTGAAC  
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CCCCAGAAATAAAATGGTATAAAATGGAATACCCCTTGAGTCCAATCACACAA  
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CTGTGGATTCTTACCAGTACGGCACCACTCAAACGCTGACATGTACGGTCTATG  
CCATTCTCCCCCGCATCACATCCACTGGTATTGGCAGTTGGAGGAAGAGTGC  
GCCAACGAGCCCAGCCAAGCTGTCTCAGTGACAAACCCATAACCTTGTGAAGA  
ATGGAGAAGTGTGGAGGACTTCCAGGGAGGAAATAAAATTGAAGTTAATAAAA  
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AGCGGCAAAATGTGTCAGCTTTGTACAAATGTGAAGCGGTCAACAAAGTCGGGA  
GAGGAGAGAGGGTGATCTCTTCCACGTGACCAGGGGTCTTGAAATTACTTTG  
CAACCTGACATGCAGCCCACTGAGCAGGAGAGCGTGTCTTTGTGGTGCATGCT  
AGACAGATCTACGTTTGAGAACCTCACATGGTACAAGCTTGGCCACAGCCTCT  
GCCAATCCATGTGGGAGAGTTGCCACACCTGTTTGCAAGAACTTGGATACTCT  
TTGGAAATTGAATGCCACCATGTTCTCTAATAGCACAAATGACATTTTGATCATG  
GAGCTTAAGAATGCATCCTTGACAGGACCAAGGAGACTATGTCTGCCTTGCTCAA  
GACAGGAAGACCAAGAAAGACATTGCGTGGTCAGGCAGCTCACAGTCCTAGA  
GCGTGTGGCACCCACGATCACAGGAAACCTGGAGAATCAGACGACAAGTATTG  
GGGAAAGCATCGAAGTCTCATGCACGGCATCTGGGAATCCCCCTCCACAGATC  
ATGTGGTTTAAAGATAATGAGACCCTTGTAGAAGACTCAGGCATTGTATTGAAG  
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TCTACACCTGCCAGGCATGCAGTGTCTTGGCTGTGCAAAAGTGGAGGCATTTT  
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GCACGGCGGTGATTGCCATGTTCTTCTGGCTACTTCTTGTCTATCATCCTACGGA  
CCGTTAAGCGGGCCAATGGAGGGGAACTGAAGACAGGGTACCTGTCCATCGT  
CATGGACCCAGATGAACTCCCATTTGGATGAACATTGTGAACGACTGCCTTATGA  
TGCCAGCAAATGGGAATTCCCAGAGACCGGCTGAAGCTAGGTAAGCCTCTTG  
GCCGTGGTGCCTTTGGCCAAGTGATTGAAGCAGATGCCTTTGGAATTGACAAG  
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CCATCTCAATGTGGTCAACCTTCTAGGTGCCTGTACCAAGCCAGGAGGGCCAC  
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GCAAGAGAAATGAATTTGTCCCCTACAAGACCAAAGGGGCACGATTCCGTCAA  
GGGAAAGACTACGTTGGAGCAATCCCTGTGGATCTGAAACGGCGCTTGGACAG

FIGURE 1B

CATCACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTTGTGGAGGAGAAGTCCC  
TCAGTGATGTAGAAGAAGAGGAAGCTCCTGAAGATCTGTATAAGGACTTCCTG  
ACCTTGGAGCATCTCATCTGTTACAGCTTCCAAGTGGCTAAGGGCATGGAGTTC  
TTGGCATCGCGAAAGTGTATCCACAGGGACCTGGCGGCACGAAATATCCTCTT  
ATCGGAGAAGAACGTGGTTAAAATCTGTGACTTTGGCTTGGCCCGGGATATTTA  
TAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGAT  
GGCCCCAGAAACAATTTTTGACAGAGTGTACACAATCCAGAGTGACGTCTGGT  
CTTTTGGTGTGTTTGTCTGTGGGAAATATTTTCCTTAGGTGCTTCTCCATATCCTGG  
GGTAAAGATTGATGAAGAATTTTGTAGGCGATTGAAAGAAGGAACTAGAATGA  
GGGCCCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGG  
CACGGGGAGCCCAGTCAGAGACCCACGTTTTTCAGAGTTGGTGGAACATTTGGG  
AAATCTCTTGCAAGCTAATGCTCAGCAGGATGGCAAAGACTACATTGTTCTTCC  
GATATCAGAGACTTTGAGCATGGAAGAGGATTCTGGACTCTCTCTGCCTACCTC  
ACCTGTTTCCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCATTATGA  
CAACACAGCAGGAATCAGTCAGTATCTGCAGAACAGTAAGCGAAAGAGCCGGC  
CTGTGAGTGTA AAAACATTTGAAGATATCCCGTTAGAAGAACCAGAAGTAAAAG  
TAATCCCAGATGACAACCAGACGGACAGTGGTATGGTTCTTGCCTCAGAAGAG  
CTGAAAACCTTTGGAAGACAGAACC AAATTATCTCCATCTTTTGGTGGAATGGTG  
CCCAGCAAAAGCAGGGAGTCTGTGGCATCTGAAGGCTCAAACCAGACAAGCG  
GCTACCAGTCCGGATATCACTCCGATGACACAGACACCACCGTGTACTCCAGT  
GAGGAAGCAGAACTTTTAAAGCTGATAGAGATTGGAGTGCAAACCGGTAGCAC  
AGCCCAGATTCTCCAGCCTGACTCGGGGACCACACTGAGCTCTCCTCCTGTTTA  
A

MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQR  
DLDWLWPNNQSGSEQRVEVTECSDGLFCKTLTIPKVI GNDTGAYKCFYRETDLAS  
VIYVYVQDYRSPFIASVSDQHGVVYTENKNKTVVIPCLGSISNLNVSLCARYPEKR  
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VLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKLVNRDLKTQS  
GSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGM  
ESLVEATVGERVRIPAKYLGYPPEIKWYKNGIPLESNHTIKAGHVLTIMEVSERDT  
GNYTVILTNPISKEKQSHVVSLVYVPPQIGEKSLISPVDSYQYGTTQTTLCTVYAI  
PPHHIHWYWQLEEECANEPSQAVSVTNPYPCEEWRSVEDFQGGNKIEVNKNQFA  
LIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPEITLQPDMP  
TEQESVSLWCTADRSTFENLTWYKLGPOPLPIHVGE LPTPVCKNLDTLWKL NATM  
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LENQTTSIGESIEVSCTASGNPPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRVRK  
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VKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRG  
AFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNV  
NLLGACTKPGGPLMVIVFECKFGNLSTYLRSKRNEFVPYKTKGARFRQGDYVG  
AIPVDLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFTLEHLICYSFQ  
VAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDAR  
LPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGT  
RMRAPDYTTPEMYQTMLDCWHGEP SQRPTFSELVEHLGNLLQANAQQDGDYTVL  
PISETLSMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVS  
VKTFEDIPL EEPEVKVIPDDNQTD SGMVLASEELKTLEDRTKLSPSFGGMVPSKSRE  
SVASEGSNQTSQGYQSGYHSDDTDTTVYSSEEAE LLKLEIGVQTGSTAQILQPDSGT  
TLSSPPV



FIGURE 3A

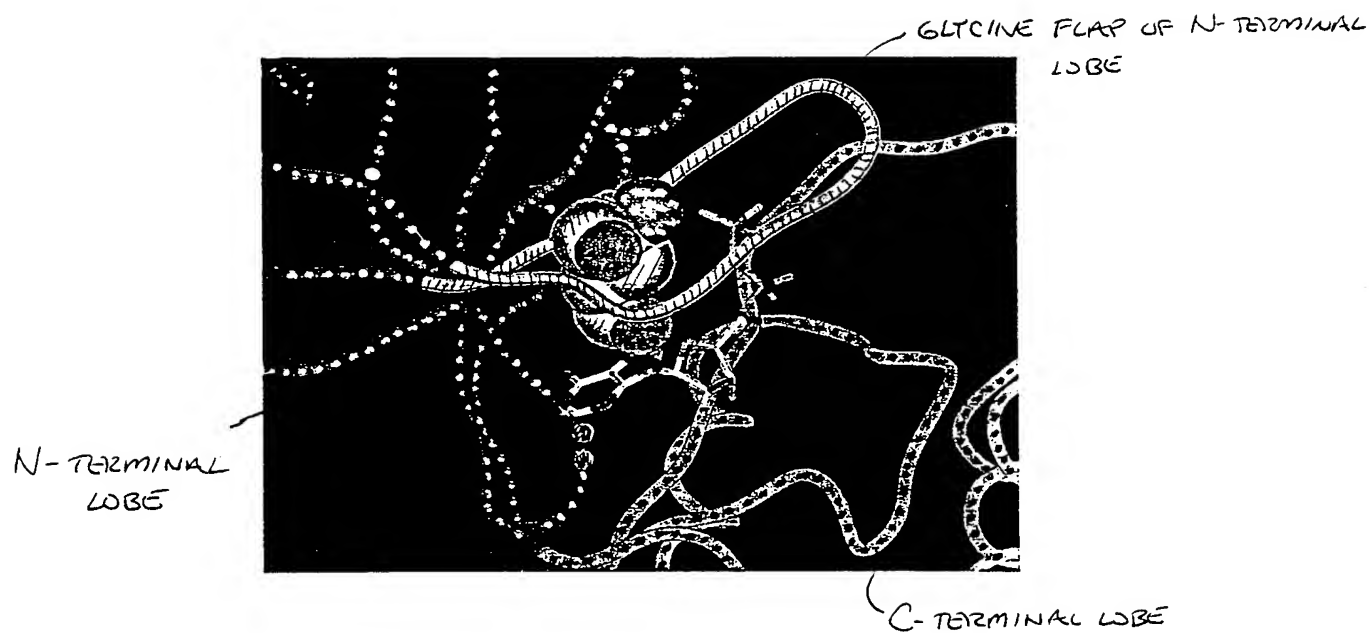


FIGURE 3B

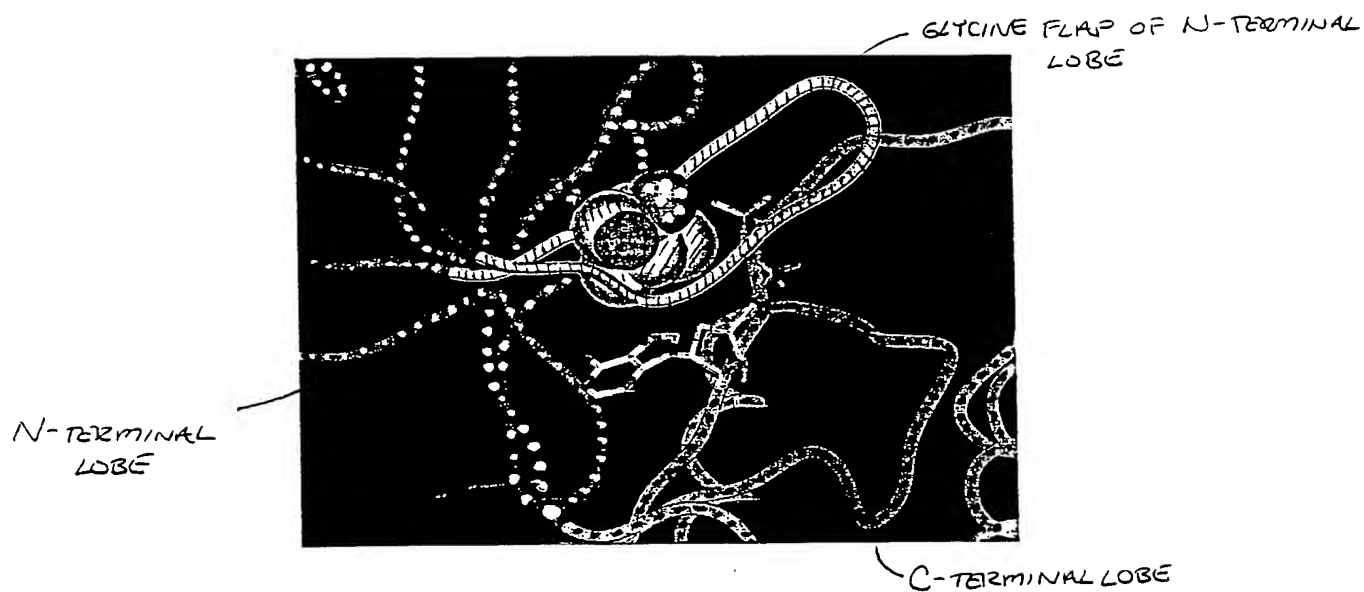


FIGURE 4A

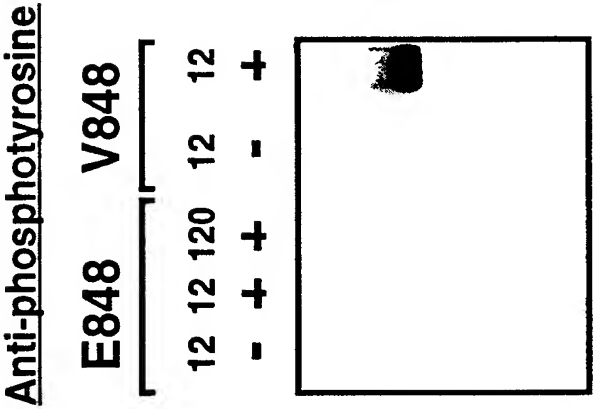
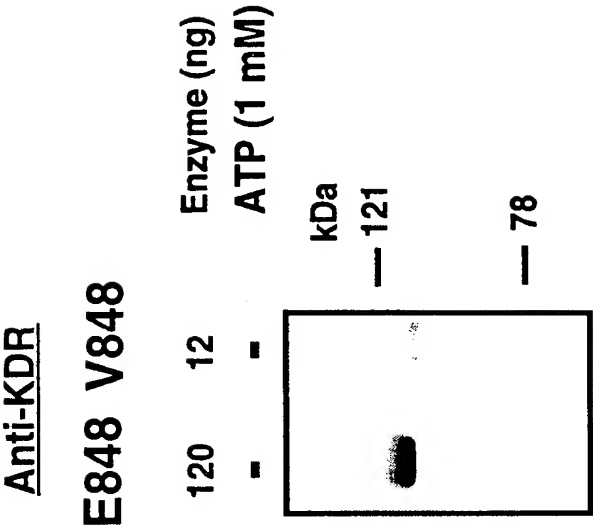


FIGURE 4B



## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12569**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : Please See Extra Sheet.

US CL : Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/194, 69.1, 252.3, 320.1, 325, 361; 436/501; 530/350; 536/23.2, 23.5.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS; STN FILES - Medline, Caplus, Wpids, Biosis, Biotechds, Scisearch. Search terms included : receptor tyrosine kinase (RTK), human KDR and growth factor?.

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category* | Citation of document, with indication, where appropriate, of the relevant passages   | Relevant to claim No. |
|-----------|--|-----------------------|
| Y         | TERMAN B. I. Identification of a new Endothelial Cell Growth Factor Receptor Tyrosine Kinase. Oncogene 1991. Vol 6. pages 1677-1683. See Table 1 and Figures 1-3.                                  | 1-40                  |
| Y         | TERMAN B. I. Identification of the KDR Tyrosine Kinase as a Receptor for Vascular Endothelial Cell growth Factor. Biochem. Biophys. Res. Com. 30 September 1992. Vol. 187. No. 3. pages 1579-1586. | 1-40                  |
| A, P      | US 5,766,860 A (TERMAN ET AL.) 16 June 1998, see Figure 7 (A-M), claim 1 in column 43 & 44.  | 41-46                 |



Further documents are listed in the continuation of Box C.



See patent family annex.

|   |  |
|---|--|
| * Special categories of cited documents:  | *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention  |
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| *E* earlier document published on or after the international filing date  | *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | *G* document member of the same patent family  |
| *O* document referring to an oral disclosure, use, exhibition or other means  |  |
| *P* document published prior to the international filing date but later than the priority date claimed  |  |

Date of the actual completion of the international search

14 AUGUST 1998

Date of mailing of the international search report

08 SEP 1998

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# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US98/12569

## A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C12N 9/12, 1/20, 15/00; G01N 33/53; C07K 1/00; C07H 21/04.

## A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

435/194, 69.1, 252.3, 320.1, 325, 361; 436/501; 530/350; 536/23.2, 23.5.